

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1214	100.0	224	2	AAW51119	Human epe
2	1214	100.0	224	2	AAW06511	Human epe
3	1214	100.0	224	3	AAW94654	Human hom
4	1214	100.0	224	9	ADY18068	PRO poly
5	1000	82.4	334	2	AAW51121	Mouse epe
6	1000	82.4	224	3	AAW94655	Marine ho
7	993	81.8	224	2	AAW51120	Rat expend
8	490	40.4	210	6	ABR40123	Human cel
9	88	7.2	931	8	ADL72200	Mouse sal
10	84.5	7.0	211	4	AAO12630	Human pol
11	84	6.9	426	4	ABW70789	N. magada
12	83	6.8	337	6	ABU56407	Mycobacte
13	83	6.8	338	2	AAAR11296	Recombina
14	83	6.8	338	2	AAW18165	Mycobacte
15	83	6.8	338	2	AAW63033	Mycobacte
16	83	6.8	338	2	AAW14852	Antigen 8
17	83	6.8	338	2	AAW14854	Antigen 8
18	83	6.8	338	4	AAW82789	Mycobacte
19	83	6.8	338	4	AAW47555	Ag85A, 12
20	83	6.8	338	5	AAW50729	Mycobacte
21	83	6.8	338	5	ABW73458	M tuberclu
22	83	6.8	338	5	ABW73460	M bovis 8
23	83	6.8	338	7	AAE39295	M. tubercl

DR N-PSDB; AAV07200.

XX New isolated endymidin-like protein - used to develop products for

PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia

PT or cerebellar degeneration.

XX

XX Claim 2, 9, 10; Fig 1A-1D; 147pp; English.

XX

CC The present sequence represents the human endymidin-like protein. The

CC invention also claims for the rat endymidin-like protein (AAW51120) and

CC its corresponding cDNA (AAV07201), and the mouse endymidin-like protein

CC (AAW51121) and its corresponding cDNA (AAV07202). The endymidin-like

CC proteins of the invention are claimed to have nerve-extending activity,

CC neuro-regenerative activity in the central nervous system, gliocyte

CC stimulating activity or memory forming activity. These endymidin-like

CC proteins and the corresponding DNA sequences which encode them are also

CC claimed to be useful as therapeutic or prophylactic agents for

CC Alzheimer's disease, Parkinson's disease, Huntington's disease,

CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration

XX

XX Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 7.2e-124;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQWYQSSG 60

DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQWYQSSG 60

QY 61 RNSRALLSYDGLNQRVRVLDERKALPCKRLFFYLLYKDGVMFQIDQATKQCSKMTLTQ 120

DB 61 RNSRALLSYDGLNQRVRVLDERKALPCKRLFFYLLYKDGVMFQIDQATKQCSKMTLTQ 120

QY 121 PWDPLDIPQNSTFEDQYSGGQEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180

DB 121 PWDPLDIPQNSTFEDQYSGGQEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180

QY 181 INYSVILSTRFFDIQLGKDPSVFTPTSTCMAQLKMSDCSW 224

DB 181 INYSVILSTRFFDIQLGKDPSVFTPTSTCMAQLKMSDCSW 224

RESULT 2

AAV06511

ID AAV06511 standard; protein; 224 AA.

XX

AC AAY06511;

XX

DT 08-OCT-1999 (first entry)

XX

DE Human endymidin.

XX

KW Endymidin; human; Parkinson's disease; Alzheimer's disease; epilepsy;

KW amyotrophic lateral sclerosis; pain; stroke; depression; anxiety;

KW neurological disorder; psychiatric disorder; cancer; therapy; diagnosis.

XX

OS Homo sapiens.

XX

FH Key

FT Peptide 1..37

FT Domain 18..28

FT Protein 38..224

FT Domain 38..47

FT Peptide 45..53

FT Peptide 56..64

FT Peptide 68..77

FT Peptide 101..107

FT Peptide 106..114

FT Peptide 113..119

FT Peptide 123..144

FT Peptide 125..142

FT Modified-site 130

FT Domain 143..154

FT Peptide 150..160

FT Domain 166..180

FT Peptide 168..176

FT Modified-site 182

FT Domain 187..193

FT Peptide 196..204

FT Domain 199..221

FT Peptide 215..223

XX WO9936565-A1.

XX 22-JUL-1999.

XX 13-JAN-1999; 99WO-US000818.

XX 14-JAN-1998; 98US-0071330P.

XX 19-FEB-1998; 98US-0075278P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ebner R;

XX WPI: 1999-458471/38.

XX N-PSDB; AAX87343.

XX A novel human endymidin and related nucleic acids, useful for treating

XX and diagnosis of nervous system-related disorders.

XX Claim 1; Page 76-77; 90pp; English.

XX This sequence represents human endymidin, a novel member of the endymidin

XX family. It was deduced from a cDNA clone (see AAX87343) discovered in a

XX primary dendritic cell cDNA library. Additional clones have been obtained

XX from KWH2, placenta, foetal and adult liver, spinal core, osteoclastoma,

XX cerebellum, synovial fibroblast, 12-week human embryo, adrenal gland

XX tumour, whole brain, Hodgkin's lymphoma, macrophage, HEL cell and

XX chondrosarcoma cDNA libraries. Endymidin polynucleotides, polypeptides

XX (including the full-length or mature polypeptide, epitope-bearing

XX polypeptides, and modified endymidin), vectors and host cells are

XX provided, as well as methods for identifying agonists and antagonists of

CC endpdymin activity. Human endpdymin can be used to treat conditions in
CC patients having need of the endpdymin protein. Conditions that can be
CC treated or detected are nervous system-related disorders, such as
CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,
CC pain, stroke, depression, anxiety, epilepsy and other neurological or
CC psychiatric disorders. Diagnosis of cancers of the nervous system is also
CC included. Endpdymin, or its agonists or antagonists may also be used to
CC treat disorders of the blood-brain barrier since endpdymin participates
CC in the endothelial cell barrier by modulating cell-matrix interactions.
CC Antagonists may inhibit formation of endpdymin-collagen fibrils, which
CC cover endothelial cells of numerous blood vessels, hence anti-endpdymin
CC antibodies may regulate angiogenesis
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.2e-124;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPCAPQAPQWEGRVQWYQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPCAPQAPQWEGRVQWYQSSG 60
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGKIDPVSFTPTSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGKIDPVSFTPTSTCQMAQLEKMSDCSW 224

RESULT 3
AAY94654
ID AAY94654 standard; protein; 224 AA.
XX AAY94654;
AC AAY94654;
XX
DT 29-AUG-2000 (first entry)
XX
DE Human homology to endpdymin-like protein (HELP) amino acid sequence.
XX
KW Homology to endpdymin-like protein; HELP; chromosome 7p14-12;
KW central nervous system disorder; peripheral nervous system disorder;
KW Alzheimer's disease; memory loss; stroke; neuronal damage;
KW osteoblast differentiation; proliferation; stimulation; bone wear;
KW arthritis; osteoporosis; cerebral cavernous malformation;
KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.
XX

OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..37
FT /label= Putative signal peptide
FT Protein 38..224
FT /label= Homology to endpdymin-like protein
XX
XX WO200032746-A2.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028341.
XX
XX 30-NOV-1998; 98US-00201442.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Pan Y;
PI
XX

DR WPI; 2000-412299/35.
DR N-PSDB; AAA27982.
XX
PT New nucleic acid molecules, designated NEL, useful for treating
PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and
PT neuronal damage (e.g. stroke).
XX
PS
XX Claim 9; Fig 4; 97pp; English.
XX
CC This sequence represents a human homology to endpdymin-like protein
CC (HELP) amino acid sequence. Endpdymin is a protein that is involved in
CC memory and neuronal regeneration. The human HELP gene is located on
CC chromosome 7p14-12. Northern analysis of HELP expression showed that an
CC approximately 3kb HELP transcript is expressed in the brain, heart, and
CC skeletal muscle. HELP is a secreted protein. Modulators of HELP
CC expression or activity can be used to treat disorders of the central
CC nervous system or peripheral nervous system, e.g. neuronal disorders,
CC memory associated disorders, such as Alzheimer's disease or stroke, or to
CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of
CC HELP expression or activity may be useful for modulation of osteoblast
CC differentiation, stimulation or proliferation. They may also be used to
CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders
CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.
CC The present invention also relates to a secreted protein with homology to
CC netrin, called netrin like protein or NEL. NEL is also referred to as
CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of
CC NEL include interacting with the protein encoded by deleted in colorectal
CC cancer, modulation of axon growth, migration and development, modulation
CC of development of the nervous system, and modulation of the guidance of
CC central nervous system commissural axons and peripheral motor axons
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 1214; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.2e-124;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPCAPQAPQWEGRVQWYQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPCAPQAPQWEGRVQWYQSSG 60
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGKIDPVSFTPTSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGKIDPVSFTPTSTCQMAQLEKMSDCSW 224

RESULT 4
ADY18068
ID ADY18068 standard; protein; 344 AA.
XX
AC ADY18068;
XX
XX 05-MAY-2005 (first entry)
XX
XX PRO polypeptide SEQ ID NO 3874.
XX
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; diagnosis.
XX
OS Homo sapiens.
XX
XX WO2005016962-A2.
PN

XX PD 24-FEB-2005.
XX PF 11-AUG-2004; 2004WO-US026249.
XX PR 11-AUG-2003; 2003US-0493546P.
XX (GETH) GENENTECH INC.
XX PI Abbas A, Clark H, Ouyang W, Williams MF, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX Claim 8; SEQ ID NO 3874; 158pp; English.
XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.
XX Sequence 344 AA;
SQ
Query Match 100.0%; Score 1214; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.3e-123;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQOSSG 60
DB 121 MGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQOSSG 180
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCKMTLTQ 120
DB 181 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCKMTLTQ 240
QY 121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSARSYETWIGIYTVKDCYPVQETFT 180
DB 241 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSARSYETWIGIYTVKDCYPVQETFT 300
QY 181 INYSVILSTRFFDIQIGKDPSPVFTPPSTCOMAQLEKMSDCSW 224
DB 301 INYSVILSTRFFDIQIGKDPSPVFTPPSTCOMAQLEKMSDCSW 344
RESULT 5
AAW51121
ID AAW51121 standard; protein; 224 AA.
XX AAW51121;
XX 06-NOV-1998 (first entry)
XX Mouse ependymin-like protein.
XX Mouse ependymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.
XX Mus sp.
XX Key Location/Qualifiers
FH 1. .37
FT /notes="Signal peptide; This sequence is claimed by the
FT inventors under claim 10 in the specification"
FT 38. .224
FT /notes="Mouse ependymin-like protein; This sequence is
FT claimed by the inventors under claim 2 in the
FT specification"

XX WO9811130-A2.
XX 19-MAR-1998.
XX 10-SEP-1997; 97WO-JP003194.
XX 11-SEP-1996; 96JP-00240880.
PR 28-NOV-1996; 96JP-00318049.
XX 27-MAY-1997; 97JP-00135633.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Ogi K, Onda H;
XX WPI; 1998-250952/22.
DR N-PSDB; AAV07202.
XX New isolated ependymin-like protein - used to develop products for
PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia
PT or cerebellar degeneration.
XX Claim 2, 9, 10; Fig 3A-3D; 147pp; English.
XX The present sequence represents the mouse ependymin-like protein. The
CC invention also claims for the rat ependymin-like protein (AAW51120) and
CC its corresponding cDNA (AAV07201), and the human ependymin-like protein
CC (AAW51119) and its corresponding cDNA (AAV07200). The ependymin-like
CC proteins of the invention are claimed to have nerve-extending activity,
CC neuro-regenerative activity in the central nervous system, gliocyte
CC stimulating activity or memory forming activity. These ependymin-like
CC proteins and the corresponding DNA sequences which encode them are also
CC claimed to be useful as therapeutic or prophylactic agents for
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration
XX Sequence 224 AA;
SQ
Query Match 82.4%; Score 1000; DB 2; Length 224;
Best Local Similarity 80.3%; Pred. No. 1.9e-100;
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;
QY 1 MGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQOSSG 60
DB 1 MGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQOSSG 60
QY 61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIDQATKQCKMTLTQ 120
DB 61 HNNRALVSVDGLNQVRVLDERKALIPCKRLFEYLLYKDGVMFQIEQATKQCAKIPLVE 120
QY 121 PWDPLDIPONSTFEDQYSIGGPOEQITVQWSDRSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 SMDPLDIPONSTFEDQYSIGGPOEQILVQWSDRRARSYETWIGYTAKDCYPVQETFI 180
QY 181 INYSVILSTRFFDIQIGKDPSPVFTPPSTCOMAQLEKMSDCS 223
DB 181 RNYTVMSTRFFDVQLGKDPSPVFTPPSTCOMAQLEKMSDCS 223
RESULT 6
AAW94655
ID AAW94655 standard; protein; 224 AA.
XX AAW94655;
XX 29-AUG-2000 (first entry)
XX Murine homology to ependymin-like protein (HELP) amino acid sequence.
XX Homology to ependymin-like protein; HELP; Alzheimer's disease; stroke;
KW central nervous system disorder; peripheral nervous system disorder; NEU;
KW neuronal damage; memory loss; osteoblast differentiation; proliferation;
KW stimulation; bone wear; arthritis; osteoporosis; netrin like protein;

CC magadii, for production of proteins and other polymers (e.g.
CC poly(hydroxybutyrate)). Vectors containing (1) allow controlled,
CC inducible expression of compounds in Archaea. (Updated on 06-AUG-2003 to
CC correct OS field.)

XX
SQ Sequence 426 AA;

Query Match 6.9%; Score 84; DB 4; Length 426;
Best Local Similarity 23.3%; Pred. No. 8.6;
Matches 42; Conservative 29; Mismatches 80; Indels 30; Gaps 9;

QY 48 WEGQVMYQSSGRNSRALLSYDGLNQRVVLDERKALIPCKLFEYILLYKDGVMFQID 107

DB 192 WASDEDMGIANGVN---VDDYDSVDEAMDVAHEVAGYVPSGGLMIVDASDD-----D 242

QY 108 QATKQCKMTLTQPW-DPL--DIPQNSTFEDQYSIGPQEQITVQEWSDRKSARSYETWI 164

DB 243 LAAYQLGKFAVSEFWNLWNLPAGETVSK--NVGDPEQGTFFEGGDEAGEGPNNVLI 300

QY 165 GIYTVKDCYVQETFTINYSVILSTRFFDLGKIDPSVFTPESTCQMAQLE-----KMSE 220

DB 301 ---DVSDANRVNAVITAGADSDTSFFDIRR-----TKVYTAEMLELDLESQVSD 348

QY 221 D 221

DB 349 D 349

RESULT 12

ABU56407
ID ABU56407 standard; protein; 337 AA.

XX AC ABU56407;

XX DT 31-MAR-2003 (first entry)

XX DE Mycobacterium tuberculosis 32kDa protein.

XX KW Antibacterial; tuberculosis; vaccine; gene therapy; 32kDa protein.

XX OS Mycobacterium tuberculosis.

XX PN US2002131975-A1.

XX PD 19-SEP-2002.

XX PF 14-SEP-2001; 2001US-00953510.

XX PR 23-NOV-1993; 93US-00156358.

XX PR 12-AUG-1994; 94US-00289667.

XX PR 23-MAY-1995; 95US-00447398.

XX PR 31-OCT-1995; 95US-00551149.

XX PR 06-DEC-1995; 95US-00568357.

XX PR 23-MAY-1996; 96US-00652842.

XX PR 21-SEP-1998; 98US-00157689.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Horwitz MA, Harth G;

XX XX WPI; 2003-174073/17.

XX DR N-PSDB; ABX75989.

XX XX New vaccine, useful for promoting an immune response against infectious
XX PT pathogens of the genus Mycobacterium in a mammalian host.
XX PS Example 1; Page 15-16; 82pp; English.

XX XX The invention describes a vaccine for promoting an immune response, in a
XX CC mammalian host, against infectious pathogens of the genus Mycobacterium,
XX CC comprising at least 1 immunodominant epitope of at least one majority
XX CC abundant extracellular product comprising Mycobacterium tuberculosis 110,
XX CC 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14, 12 kD protein or

CC their analogues, homologues or subunits. The proteins and polypeptides of
CC the invention are useful in gene therapy and treatment of diseases caused
CC by Mycobacterium such as tuberculosis. This is the amino acid sequence of
CC the Mycobacterium tuberculosis 32kDa protein

XX SQ Sequence 337 AA;

Query Match 6.8%; Score 83; DB 6; Length 337;
Best Local Similarity 40.0%; Pred. No. 7.8;
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;

QY 8 RTVPGLGALWLLGGLWANTLGLCSLGAVGAP-----RPGCAPQQWGRQVMYQ-QSSGRN 62

DB 17 RLIVGVAGAAALVSGL-VGAVGGTATAGAFSRPGLPVEYLQVPSMGRDIKVFQSGGAN 75

QY 63 SRALLSYDGL 72

DB 76 SPALYLLDGL 85

RESULT 13

AAR11296

ID AAR11296 standard; protein; 338 AA.

XX AC AAR11296;

XX DT 25-MAR-2003 (revised)

XX DT 30-MAY-1991 (first entry)

XX DE Recombinant M.tuberculosis 32kD antigen.

XX KW tuberculosis; vaccine; BCG; antigen.

XX OS Mycobacterium tuberculosis.

XX FH Key Location/Qualifiers

XX FT Peptide 1..43

XX FT Protein 44..338

XX FT /label= tuberculosis 32kD antigen

XX PN EP419355-A.

XX XX 27-MAR-1991.

XX XX 19-SEP-1990; 90EP-00402590.

XX XX 19-SEP-1989; 89EP-00402571.

XX XX (INNO-) INNOGENETICS NV SA.

XX XX Content J, Dewit L, Debruyne J, Vanvooren JP;

XX XX WPI; 1991-088933/13.

XX XX N-PSDB; AAQ11082.

XX PT Polypeptide comprising recombinant polypeptide - with defined peptide

XX PT sequence(s) used for diagnosis and for preparing vaccine against

XX PT tuberculosis.

XX PS Claim 3; Fig 5; 134pp; English.

XX CC Polyclonal antiserum was raised in rabbits to the 32kD protein of M.

XX CC bovis BCG. The antiserum was then used to screen a lambda gt11

XX CC recombinant DNA library constructed from genomic DNA of M. tuberculosis

XX CC (Erdman strain). Positive clones were analysed and sequenced. The deduced

XX CC amino-terminal amino acid sequence of the mature protein corresponds to

CC 2003 to correct PI field.)
XX
SQ Sequence 338 AA;

Query Match 6.8%; Score 83; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 7.9;
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;

QY 8 RTVPGLGAWLLGGLMAWTLCGLCSLGAAGAP---RPCOAPQOWEGROVMYQ-QSSGRN 62
Db 17 RLTVGAVGAALVSGL-VGAVGGTATAGAFRRPGLPVEYLQVPSMGRDIKVFQSGGAN 75

QY 63 SRALLSYDGL 72
Db 76 SPALYLLDGL 85

RESULT 14
AAW18165
ID AAW18165 standard; protein; 338 AA.
XX
AC AAW18165;
XX
DT 13-AUG-1997 (first entry)
XX
DE Mycobacterium tuberculosis extracellular 32AKD protein.
XX
KW Vaccine; vaccinating agent; M.tuberculosis; pathogen; bacteria; virus;
KW fungus; protozoan; HIV.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT Protein 44..338
FT /label= Mature
XX
PN WO9637219-A1.
XX
PD 28-NOV-1996.
XX
PF 23-MAY-1996; 96WO-US007781.
XX
PR 23-MAY-1995; 95US-00447398.
PR 20-OCT-1995; 95US-00545926.
PR 31-OCT-1995; 95US-00551149.
PR 06-DEC-1995; 95US-00568357.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Horwitz MA, Harth G;
XX
DR WPI; 1997-020936/02.
DR N-PSDB; AAT71599.
XX
PT Vaccines derived from M.tuberculosis major abundant extracellular
PT proteins - are easy to prepare and less toxic than conventional killed or
PT attenuated vaccines, useful for protecting against or treating
PT Mycobacterial infections.
XX
PS Claim 1; Page 36-38; 193pp; English.
XX
CC A vaccinating agent for promoting an immune response in a mammal against
CC Mycobacterium pathogens comprises at least one majorly abundant
CC extracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45, 32A,
CC 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their analogues,
CC homologues and subunits. The present sequence represents the 32A kD
CC protein. The vaccinating agents are used to protect against (or to treat
CC existing) infections by Mycobacterium (especially M. tuberculosis) while
CC the epitopes can also be used to detect presence of an immune response to
CC a Mycobacterium pathogen. The vectors, containing the DNA for the
CC extracellular proteins, are used to transform cells for production of
CC recombinant DNA molecules. More generally the DNA from other pathogens
CC can be used in vaccines, e.g. against other bacteria, viruses, fungi and

CC protozoa. Since different combinations of DNA can be used, a wide range
CC of effective compositions can be produced. They generate a response
CC against the antigens most often found on infected cells during the
CC infection, regardless of the strength or specificity of the immune
CC response. The vaccines are easy to produce and less toxic than known
CC killed or attenuated vaccines, so can be given to immunocompromised
CC subjects, e.g. those with HIV infection
XX
SQ Sequence 338 AA;

Query Match 6.8%; Score 83; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 7.9;
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;

QY 8 RTVPGLGAWLLGGLMAWTLCGLCSLGAAGAP---RPCOAPQOWEGROVMYQ-QSSGRN 62
Db 17 RLTVGAVGAALVSGL-VGAVGGTATAGAFRRPGLPVEYLQVPSMGRDIKVFQSGGAN 75

QY 63 SRALLSYDGL 72
Db 76 SPALYLLDGL 85

RESULT 15
AAW63033
ID AAW63033 standard; protein; 338 AA.
XX
AC AAW63033;
XX
DT 23-OCT-1998 (first entry)
XX
DE Mycobacterium tuberculosis 32 kD protein sequence.
XX
KW Mycobacterium tuberculosis; vaccination; extracellular product;
KW immunodominant epitope; interleukin-12; MF59; immune response;
KW opsonising humoral response; intracellular pathogen.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9831388-A1.
XX
PD 23-JUL-1998.
XX
PF 15-JAN-1998; 98WO-US000942.
XX
PR 21-JAN-1997; 97US-00786533.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Horwitz MA, Harth G, Lee B;
XX
DR WPI; 1998-413815/35.
DR N-PSDB; AAV42596.
XX
PT Vaccines against Mycobacterium containing major extracellular proteins -
PT used to, e.g. induce protective and therapeutic immune responses, and for
PT detecting an immune response.
XX
PS Example 2; Page 38-40; 236pp; English.
XX
CC This represents a Mycobacterium tuberculosis 32 kD protein. The invention
CC provides an agent for vaccinating mammals against Mycobacterium. The
CC agent comprises at least one of the major abundant extracellular 110, 80,
CC 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins of M.
CC tuberculosis, or at least 1 of their immunodominant epitopes and
CC interleukin-12 (IL-12) or MF59 as adjuvants. The agent containing the
CC nucleic acid encoding the extracellular products are used to raise a
CC protective or therapeutic immune response against Mycobacterium,
CC specifically M. tuberculosis. The immunodominant epitopes can also be
CC used (typically in a cutaneous hypersensitivity test) to detect an immune
CC response to vaccination. Preparation of the agent does not require
CC selection of the most immunogenic products, so large scale production and
CC purification are easy, resulting in a consistent, standardised

CC formulation, having lower toxicity than killed or attenuated vaccines.
CC The agents provide a rapid and effective response (including a strong
CC cell-mediated component) and are safe even in immunocompromised subjects.
CC They prevent development of an opsonising humoral response that might
CC spread intracellular pathogens
XX
SQ Sequence 338 AA;

Query Match 6.8%; Score 83; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 7.9;
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;
QY 8 RTVPGALGAWLLGGLHAWTLGCLSLGAVGAP----RPCOAPQOWEGRQVWYQ-QSSGRN 62
DB 17 RLVVGAVGAALVSGL-VGAVGGTATAGAFSRPGLPVEYLQVPSPSMGRDVKVQFQSGGAN 75
QY 63 SRALLSYDGL 72
DB 76 SPALYLLDGL 85

Search completed: June 10, 2006, 02:51:52
Job time : 205 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 10, 2006, 02:52:09 ; Search time 41 Seconds
(without alignments)
525.672 Million cell updates/sec

Title: US-10-733-646-2
Perfect score: 1214
Sequence: 1 MPCRPLRTVPGALGAWLLG.....TPSTCQMAQLEKMSDECSW 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	192.5	15.9	221	2 JC1251	ependymin Om-II pr
2	190.5	15.7	221	2 JC1250	ependymin Om-I pre
3	185.5	15.3	221	2 I50538	ependymin - northe
4	167.5	13.8	215	2 I51377	ependymin precurs
5	163.5	13.5	212	2 I50490	ependymin - Atlant
6	156.5	12.9	216	2 J10090	ependymin precurs
7	154.5	12.7	217	2 A43820	ependymin precurs
8	153.5	12.6	216	2 A32636	ependymin II precu
9	87	7.2	1085	2 E70834	probable regulator
10	84	6.9	845	2 S75644	hypothetical prote
11	83	6.8	338	2 S10326	alpha-antigen A, e
12	83	6.8	338	2 H70897	32K antigen fbpA p
13	82.5	6.8	493	2 AB2434	hypothetical prote
14	80.5	6.6	957	2 T15976	hypothetical prote
15	79.5	6.5	2548	2 E59435	myosin IXA import
16	79	6.5	257	2 C97109	specialized DNA-de
17	79	6.5	257	2 I40621	probable transcrip
18	78.5	6.5	275	2 A72319	conserved hypothet
19	78.5	6.5	1541	2 S46686	hypothetical prote
20	78	6.4	288	2 I55184	repA protein - Esc
21	78	6.4	373	2 T12063	xpsL protein - Xan
22	77.5	6.4	381	2 C86358	Similar to zinc fi
23	77.5	6.4	552	2 S50313	iron transport pro
24	77.5	6.4	643	2 G64412	hypothetical prote
25	77	6.3	678	2 T05821	hypothetical prote
26	76.5	6.3	323	2 A23348	alpha-antigen B pr
27	76.5	6.3	325	2 S29663	antigen 85-B precu
28	76	6.3	295	2 T40061	hypothetical prote
29	76	6.3	325	2 A37185	alpha-antigen prec

30	76	6.3	1118	1 A49724	protein-tyrosine-p
31	75.5	6.2	600	2 H81733	DNA primase TC0175
32	75.5	6.2	686	1 E64946	oligopeptidase B (
33	75	6.2	747	1 WZBE45	gene 45 protein -
34	75	6.2	1148	2 T13347	Cnn protein - frui
35	74.5	6.1	615	2 PH0853	methyl-directed mi
36	74.5	6.1	632	2 S64786	hypothetical prote
37	74	6.1	1456	1 A36563	mannose receptor p
38	73.5	6.1	327	2 S20038	fibronectin-bindin
39	73.5	6.1	327	2 G87162	antigen 85A, mycol
40	73.5	6.1	1219	2 S54570	probable membrane
41	73.5	6.1	1720	2 T07258	cell division prot
42	73	6.0	327	1 JQ0965	chitinase (EC 3.2.
43	73	6.0	440	2 T32457	hypothetical prote
44	73	6.0	1451	2 B86286	F9L1.15 protein -
45	73	6.0	1641	2 T10955	early nodulin bind

ALIGNMENTS

RESULT 1

JC1251

ependymin Om-II precursor - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1251

R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.

Gene 118, 189-196, 1992

A:Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and

A:Reference number: JC1250; MUID:92380503; PMID:1511892

A:Accession: JC1251

A:Molecule type: mRNA

A:Residues: 1-221 <MUE>

A:Cross-references: UNIPROT:P28771; UNIPARC:UPI000012A096; GB:M93698; NID:g213413; PID:

C:Comment: This protein shares several characteristics with soluble glycoproteins medi

C:Genetics:

A:Gene: Om-II

C:Superfamily: ependymin

C:Keywords: Glycoprotein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-221/Product: ependymin Om-II #status predicted <MAT>

F:33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.9%; Score 192.5; DB 2; Length 221;
Best Local Similarity 25.0%; Pred. No. 8e-11;
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

QY 25 WTLGCLSLGAVGAPRPCAPQWEGRQVMYQQSSGRNSRALLSYDGLNQRRVLDERKA 84

Db 12 WLCGATALAESHCPOHCTSPNMTGVLTVALTGGEIKATCHYSDSTNKKLRFTESEMH 71

QY 85 LIPCKRLFEYILYKGMFOIDQATKQCSKMTLTQPDPLDIPONSTFEDQYSIGG--- 141

Db 72 LNKTEHLEDYLMFEEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV 131

QY 142 PQQGITVQWSDRSKARSYETWIGIYTVKQCPVQETFTINYSVILSTRFFDIQLGIDKP 201

Db 132 QEDNIKVINWVG-SVAETKGOYSALTTVGECPL-STFYSTDSTITLLFSNSEVTEVKAP 189

QY 202 SVFTPPSTCQMAQLEK 217

Db 190 EMETLPSFCFAVELEE 205

RESULT 2

JC1250

ependymin Om-I precursor - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1250; PC1124

R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.

Gene 118, 189-196, 1992

A;Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and md
A;Reference number: JC1250; MUID:92380503; PMID:1511892
A;Accession: JC1250
A;Molecule type: mRNA
A;Residues: 1-221 <MUE>
A;Cross-references: UNIPROT:P28770; UNIPARC:UPI000012A092; GB:M93697; NID:g213411; PIDN:
A;Accession: PC1124
A;Molecule type: protein
A;Residues: 22-44;198-221 <MU2>
A;Cross-references: UNIPARC:UPI00001788FF; UNIPARC:UPI0000178900
C;Comment: This protein shares several characteristics with soluble glycoproteins mediato
C;Genetics:
A;Gene: Om-I
C;Superfamily: ependymin
C;Keywords: glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-221/Product: ependymin Om-I #status experimental <MAT>
F;33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 15.7%; Score 190.5; DB 2; Length 221;
Best Local Similarity 24.0%; Pred. No. 1.2e-10;
Matches 50; Conservative 42; Mismatches 111; Indels 5; Gaps 3;
QY 16 AWLLGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQR 75
DB 3 AFVAALSIWLCUGATTLAESHGPHQCTSPNMTGVLTVALTGTGEIKATGHYSYDSTDKK 62
QY 76 VRVLDERKALIPCKRFLFEYLLKDGVMFOIDQATKQCKMTLTQPDPLDIPQNSTFFED 135
DB 63 IRTESEMLNKTEHLEDYLMLEEGVFYDIDMKQSKCKMSLHSHAHLELPAGAAHQV 122
QY 136 QYSIGG---PQOITVOEWSDRKSARSYETWIGIYTKDCYPVOETFTINYSVILSTRFF 192
DB 123 ELFLGSDTVOEEDIKNVIWTSVPETKGOYFLST-IVGECPL-STFYSTDSITLLFSNS 180
QY 193 DIQLGIKDPSVFTPPSTCQMAQLEKMS 220
DB 181 EVVTEVKAPEVFNLPSCFGEVELEAPE 208
RESULT 3
150538
ependymin - northern pike
C;Species: Esox lucius (northern pike)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50538
R;Mueller-Schmid, A.; Ganes, B.; Gorr, T.; Hoffmann, W.
J. Mol. Evol. 36, 578-585, 1993
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Clu
A;Reference number: I50490; MUID:93353529; PMID:8350351
A;Accession: I50538
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-221 <MUE>
A;Cross-references: UNIPROT:P32188; UNIPARC:UPI000012A09D; GB:L09066; NID:g305096; PIDN:
C;Genetics:
A;Gene: Epd
C;Superfamily: ependymin
C;Keywords: glycoprotein
F;37,77,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 15.3%; Score 185.5; DB 2; Length 221;
Best Local Similarity 27.3%; Pred. No. 3.7e-10;
Matches 59; Conservative 34; Mismatches 106; Indels 17; Gaps 6;
QY 13 ALGAWLLGLWAWTLGCLSLGAVGAPRCPQAPQWEGRVQVMYQSSGRNSRALLSYDGL 72
DB 8 ALSIWLC--LGATTLAE--SLAOSHGPQHCTSPNMTGVLTVMALNGEIKATGHYHYDTT 63
QY 73 NQRVVRVLDERKALIPCKRFLFEYLLKDGVMFOIDQATKQCKMTLTQPDPLDIPQNST 132
DB 64 DKKLRTFESMHLNKSEHLEDYLMLEEGVFYDIDLNQSKCRKWSLQSHAHALELPAGAV 123

QY 133 FEDQYSIGG---PQOITVOEW-----SDRKSARSYETWIGIYTKDCYPVOETFTINYSV 185
DB 124 HQVELFLGSDTVOEENIKVINWMSVPETKGOYSVST-----TVGDCPL-STFYSTDSI 177
QY 186 ILSTRFFDIQLGIKDPSVFTPPSTCQMAQLEKMSD 221
DB 178 TLLFNSQVTVTEKPEVEFSLFSFCGLELEDTHTND 213
RESULT 4
151377
ependymin precursor - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51377
R;Adams, D.S.; Shashoua, V.E.
Gene 141, 237-241, 1994
A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.
A;Reference number: I51377; MUID:94215910; PMID:8163195
A;Accession: I51377
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-215 <ADA>
A;Cross-references: UNIPROT:P38528; UNIPARC:UPI000012A09B; EMBL:U00432; NID:g397655; PI
C;Genetics:
A;Gene: epn
A;Introns: 28/1; 39/3; 84/3; 147/1; 175/2
C;Superfamily: ependymin
Query Match 13.8%; Score 167.5; DB 2; Length 215;
Best Local Similarity 24.4%; Pred. No. 1.9e-08;
Matches 50; Conservative 47; Mismatches 89; Indels 19; Gaps 8;
QY 30 LCSLGVAGAPR-PCQAPQWEGRVQVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALI 86
DB 14 LCVAWASSNRQPCSPPLTSG--TMKVYSTGHDLASGEFSYDSKANKRPFVEDTAHAN 71
QY 87 PKRLFEYLLKDGVMFOIDQATKQCKMTLTQPDPLDIPQNSTFEDQYSIGSP---Q 143
DB 72 KTSHM-DVLVHFEEGVLYEIDSKNESCKETLQFRKHLMEIPDPATHESIYNGSPSITE 130
QY 144 EOITVOEWSDR---KSARSYETWIGIYTKDCYPVOETFTINYSVILSTRFFDIQLGIK 199
DB 131 QGLRVRVNKGKLPHELHAHYSLSLT-----TSCGCLPVSYSYGDKKLLFS-FGVETEVD 184
QY 200 DPSVFTPPSTCQMAQLEKMSDPCSW 224
DB 185 DQGVFPVPAYCEAVAPEEAPDDHSF 209
RESULT 5
150490
ependymin - Atlantic herring
C;Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50490
R;Mueller-Schmid, A.; Ganes, B.; Gorr, T.; Hoffmann, W.
J. Mol. Evol. 36, 578-585, 1993
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Cl
A;Reference number: I50490; MUID:93353529; PMID:8350351
A;Accession: I50490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MUE>
A;Cross-references: UNIPROT:P32187; UNIPARC:UPI000012A09A; GB:L09065; NID:g304576; PIDN:
C;Genetics:
A;Gene: Epd
C;Superfamily: ependymin
C;Keywords: glycoprotein
F;69,92,112/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 13.5%; Score 163.5; DB 2; Length 212;
Best Local Similarity 24.8%; Pred. No. 4.5e-08;

Matches 50; Conservative 40; Mismatches 95; Indels 17; Gaps 8;
QY 27 LC-GLCSLGAV--GAPRPCAPQWEGQVMYQQSSGRNSRALLSYDGLNQVRVLDERK 83
Db 7 LCVALMSASAVLAELHQPCCPPQTHGNLWVTAAGAPASVGEFNYSQARKLHFKDDAL 66
QY 84 ALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQWPDLPDIPQNSTFEDQVSIIGP- 142
Db 67 HVNKTDHL-EMLIFFEEGIFYDIDSHNSCHKTKLQSTYHCLVPPNATHVTGELGSEF 125
QY 143 --QEQITVQWSDRSARSYETWIGIYTVK----DCYPVOETFTINYSVILSTRFFDIQL 196
Db 126 IGGQVRMRKW--RKRVPELD---GVTVATTCGCVTLFATLFTDSNDVLVFNFLDVM 180
QY 197 GIKDP-SVFTPPSTCQMAQLEK 217
Db 181 KVNPLEVFPPSPYCDGVALEE 202
RESULT 6
JL0090
ependymin precursor - goldfish
N;Alternate names: preproependymin
C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0090; PS0306; I51378
R;Koenigstorfer, A.; Sterrer, S.; Eckerskorn, C.; Lottspeich, F.; Schmidt, R.; Hoffmann, J. Neurochem. 52, 310-312, 1989
A;Title: Molecular characterization of an ependymin precursor from goldfish brain.
A;Reference number: JL0090; MUID:89086004; PMID:2908890
A;Accession: JL0090
A;Molecule type: mRNA
A;Residues: 1-216 <KOE>
A;Cross-references: UNIPROT:P13506; UNIPARC:UPI00001711C3; GB:X141134; NID:G62577; PIDN:Q
A;Experimental source: brain
A;Accession: PS0306
A;Molecule type: protein
A;Residues: 22-27, 'X', 29-45; I110-123 <KO2>
A;Cross-references: UNIPARC:UPI0001788FD; UNIPARC:UPI00001788FE
A;Note: ependymins beta and gamma have the same amino-terminal sequence
A;Note: 24-Asp, 29-Glu, and 34-Ile were also found
R;Adams, D.S.; Shashoua, V.E. Gene 141, 237-241, 1994
A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.
A;Reference number: I51377; MUID:94215910; PMID:8163195
A;Accession: I51378
A;Status: preliminary; translated from GB/EMBL/DBJ .
A;Molecule type: DNA
A;Residues: 2-216 <ADA>
A;Cross-references: UNIPARC:UPI000012A091; EMBL:U00433; NID:G397657; PIDN:AAA19566.1; PT
C;Comment: Ependymins beta and gamma are nervous-system specific glycoproteins localized
C;Comment: These proteins are reported as brain proteins that display enhanced turnover
C;Comment: Ependymin forms dimer with intermolecular disulfide bonds.
C;Genetics:
A;Gene: epn
A;Intons: 29/1; 40/3; 85/3; 148/1; 176/2
C;Superfamily: ependymin
C;Keywords: calcium binding; cell adhesion; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-216/Product: ependymin #status experimental <MAT>
F;72,95/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;181,183,185,186/Binding site: calcium (Glu, Asp, Asp) #status predicted
F;181,203,206,207/Binding site: calcium (Glu, Glu, Asp, Asp) #status predicted
Query Match 12.9%; Score 156.5; DB 2; Length 216;
Best Local Similarity 22.1%; Pred. No. 2.1e-07;
Matches 45; Conservative 45; Mismatches 97; Indels 17; Gaps 6;
QY 30 LCSLGAVGAPR-PCQAPQWEGQVMYQQSSGRNSRALLSYDGLNQVRVLDERKALIPC 88
Db 15 LCVAWASSHRRQCHAPPLTSGTMKVVTGCHDLSEGSFYSKANKRFREVDTAHAKNT 74
QY 89 KRLFEVILLYKDGVMFQIDQATKQCSKMTLTQWPDLPDIPQNSTFEDQVSIIGP---QE 145

Db 75 SHN-DVLIHFEEGLVEIDSKNESCKETLQFRKHLMEIPPDATHESEIYMGSPSITEQG 133
QY 146 ITVQWSDRSARSYETWIGIYTKCYPVOETP-----TINYSVILSTRFFDIQLGDK 200
Db 134 LRVVWNG-KFPELHAHYSMTTSCGCLPVSGSYHGKGLHFS-----FFGVETEVD 186
QY 201 PSVFTPPSTCQMAQLEKMSDCSW 224
Db 187 LQVFVPAYCEGVAFEEAPDDHSF 210
RESULT 7
A43820
ependymin precursor - zebra fish
N;Alternate names: proependymin
C;Species: Brachydanio rerio (zebra fish)
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C;Accession: A43820; I50104; S10454
R;Sterrer, S.; Koenigstorfer, A.; Hoffmann, W. Neuroscience 37, 277-284, 1990
A;Title: Biosynthesis and expression of ependymin homologous sequences in zebrafish bra
A;Reference number: A43820; MUID:91056885; PMID:2243597
A;Accession: A43820
A;Molecule type: mRNA
A;Residues: 1-217 <STE>
A;Cross-references: UNIPROT:P17561; UNIPARC:UPI000012A099; EMBL:X52502; NID:G62523; PID
C;Superfamily: ependymin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-217/Product: ependymin #status predicted <MAT>
Query Match 12.7%; Score 154.5; DB 2; Length 217;
Best Local Similarity 24.5%; Pred. No. 3.3e-07;
Matches 51; Conservative 44; Mismatches 90; Indels 23; Gaps 9;
QY 30 LCSLGAV---GAPRPCAPQWEGQVMYQQSSGRNSRAL--LSYDGLNQVRVLDERKA 84
Db 14 LCAIGWASSHSHRQCHSPQLTSG--TMKVVTGCHDLASGEFSYDSKTNKRFREVDTH 71
QY 85 LIFCKLFEVILLYKDGVMFQIDQATKQCSKMTLTQWPDLPDIPQNSTFEDQVSIIGP-- 142
Db 72 ANKTSYI-DVLIHFEEGLVEIDSKNESCKETLQFRKHLMEIPVDATHESEIYMGSPSL 130
QY 143 -QEQITVQWSDR--KSARSYE---TWIGIYTKCYPVOETFTINYSVILSTRFFDIQL 196
Db 131 TEQGLRVVWNGKFPPELHAHYSLTSTSCGLTVSGSY-YGEKKDLFFS-----FFGVET 183
QY 197 GIKDPSVFTPPSTCQMAQLEKMSDCSW 224
Db 184 EVDDLQVAPPAYCEGVAFEEAPDDHSF 211
RESULT 8
A32636
ependymin II precursor - goldfish
N;Alternate names: proendomycin II
C;Species: Carassius auratus (goldfish)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C;Accession: A32636
R;Koenigstorfer, A.; Sterrer, S.; Hoffmann, W. J. Biol. Chem. 264, 13689-13692, 1989
A;Title: Biosynthesis of ependymins from goldfish brain.
A;Reference number: A32636; MUID:89340451; PMID:2760037
A;Accession: A32636
A;Molecule type: mRNA
A;Residues: 1-216 <KOE>
A;Cross-references: UNIPROT:P12958; UNIPARC:UPI0000155EE6; GB:J04986; NID:G212951; PIDN
C;Superfamily: ependymin
C;Keywords: glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-216/Product: endomycin II #status predicted <MAT>
F;72,95/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match 12.6%; Score 153.5; DB 2; Length 216;
Best Local Similarity 23.3%; Pred. No. 4.1e-07;
Matches 48; Conservative 45; Mismatches 97; Indels 11; Gaps 7;

QY 30 LCSGLGAVGAPR-PCQAPQWEGRVQVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALI 86
DB 15 LCANAVASSDRQPCQSPPLISG--TWKVYSTGHDLIASGEFSYDSKANKFRFVEDAAHAN 72

QY 87 PKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQPMWDLDPONSTFEDQYSIGSP---Q 143
DB 73 KTSHT-DVLVHPEEGTLYEIDSKNESCKKTELQFRKHLMEIPDPDTHSESIYWGSPSITE 131

QY 144 EQITVQWSDRKARSYETWIGYTVKDCYVPQETTTINYSVILSTRFRFDIQLGIKDPVS 203
DB 132 QGURVRVWSGKLPELHAHYSLSI-TSCGLPLVSGSYGDKKOLLFS-FFGVETEVDLDQV 189

QY 204 FTPPSTCOMAQLKMSGDCSW 224
DB 190 FVPPAYCEGVAFEEAPDDHSF 210

RESULT 9
E70834
probable regulatory protein with some - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: E70834
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID:98295987; PMID:9634230
A: Accession: E70834
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-1085 <COL>
A: Cross-references: UNIPROT:O53720; UNIPARC:UPI000016521A; GB:AL021931; GB:AL123456; NID
A: Experimental source: strain H37Rv
C: Genetics:
A: Gene: RV0386

Query Match 7.2%; Score 87; DB 2; Length 1085;
Best Local Similarity 23.3%; Pred. No. 6.5;
Matches 67; Conservative 36; Mismatches 88; Indels 96; Gaps 16;

QY 2 PGRAPLRTVPGLGAW-----LLGGLMAWTLCGLCS-----LGAVGA 38
DB 256 PDLVPV-TVAGALGHDQGRSTTDTVLFLGGRPALVLDNCEHLLDATAALVLALVKA 314

QY 39 PR-----PCQAPQWEGRVQYQ-QSSGRNSRALLSYDGLNQRV----RVLDERKALIP 87
DB 315 CRGVRLATCREPLRVGE-EVSVRVPSLSLSDEAVEMFCYRAQVRPDRFLRTDDNSAAVT 373

QY 88 --CKRLFEYLLYKDGVMFQIDQATKQCSKMTLTQPMWDLDPONSTFEDQYSI--GGPQ 143
DB 374 EICKRL-----DGLPLAIELAAARLSMTLDEIIDGL-----RDRFALLTGGAR 417

QY 144 EQITVQ-----EWS-----DRKSARSYETWIGYTVKDCYVPV-----Q 176
DB 418 TAAHQOQTWASVDWSTLTTEPRTILFRFLAVFGVCFVDDQAQVACSGDVQRYQVLDE 477

QY 177 ETTFTINYSVILSTRFRFDIQLGIKDPVSFTPPSTCOMAQ-----LEKMS 220
DB 478 IITLVKSLVMA-----DDNSGRTCYRLCETMRHYALEKLS 514

RESULT 10
S75644
hypothetical protein sll1885 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A: Variety: PCC 6803
```

```
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75644
R: Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasui, DNA Res. 3, 109-136, 1996
A: Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.
A: Reference number: S74322; MUID:97061201; PMID:8905231
A: Accession: S75644
A: Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-845 <KAN>
A: Cross-references: UNIPROT:P74119; UNIPARC:UPI00000C1006; EMBL:D90912; GB:AB001339; NID
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C: Genetics:
A: Start codon: GTG
C: Superfamily: Synechocystis hypothetical protein sll1885

Query Match 6.9%; Score 84; DB 2; Length 845;
Best Local Similarity 19.5%; Pred. No. 9.3;
Matches 56; Conservative 42; Mismatches 103; Indels 86; Gaps 11;

QY 12 GALGAWLLGGLMAWTLCGLCSLGAVGAP-----RPC---- 42
DB 16 GILGAWLVLGANSSNTDHHGISSPSALADPPPNQKISPVFTQNDYSSISFSPATLVS 75
QY 43 QAPQWEGRVQVMYQSS-----SGRNSRALLSYDGLNQRVRLD 80
DB 76 QPSSRSGRSILMVEAEDNFALQAVTLTVDNVILHNGQQTAABELTDSRTNRLALVV 135
QY 81 ERKAL--IPCKR-----LFEYLLYKDGVMFQIDQATKQCSKMTLTQPMW---- 123
DB 136 EGVKLADSPINQDNAGPDGTLMKRLRIK-----QLDRGVVEVSLNAQEQSWTVRSHNQ 190
QY 124 -----PLDIPONS---TFEDQYSIG--GPQEQITVQWSDRKARSYETWIGYTVKDCY 173
DB 191 GILLAPTAATAETLEIKDEVSQGELSPEETLLSQTTAIDGARVEEISVETTTES-- 248
QY 174 PVQETFTINYSVILSTRFRFDIQLGIKDPVSFTPPSTCOMAQLEKMS 220
DB 249 -AONGITESSDLNQNLGDIITPIETPTISSEESTVNVLETQREND 294

RESULT 11
S10326
alpha-antigen A, extracellular - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S10326; B41499
R: de Wit, L.; de la Cuvelier, A.; Ooms, J.; Content, J.
Nucleic Acids Res. 18, 3995, 1990
A: Title: Nucleotide sequence of the 32 kDa-protein gene (antigen 85 A) of Mycobacterium
A: Reference number: S10326; MUID:90326531; PMID:2197602
A: Accession: S10326
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-338 <WIT>
A: Cross-references: UNIPROT:P17944; UNIPARC:UPI000002CE66; EMBL:X53034; NID:944165; PID
R: Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A: Title: Evidence for three separate genes encoding the proteins of the mycobacterial
A: Reference number: A41499; MUID:90093478; PMID:2403534
A: Accession: B41499
A: Status: preliminary
A: Molecule type: protein
A: Residues: 44-82 <WIK>
A: Cross-references: UNIPARC:UPI00000AP300
C: Superfamily: Mycobacterium avium alpha-antigen

Query Match 6.8%; Score 83; DB 2; Length 338;
Best Local Similarity 40.0%; Pred. No. 3.8;
Matches 28; Conservative 5; Mismatches 31; Indels 6; Gaps 3;
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C:Species: Homo sapiens (man)
C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C:Accession: E59435
C:Accession: E59435
R:Gorman, S.W.; Haider, N.B.; Grieshammer, U.; Swiderski, R.E.; Kim, E.; Welch, J.W.; Se
Genomics 59, 150-160, 1999
A:Title: The cloning and developmental expression of unconventional myosin IXA (MYO9A) a
A:Reference number: E59435
A:Accession: E59435
A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-2548 <GOR>
A:Cross-references: UNIPROT:Q9UNJ2; UNIPARC:UPI0000007206F; GB:NP_008832; PID:q5902012; E

	Query Match	6.5%; Score 79.5; DB 2; Length 2548;
	Best Local Similarity	20.2%; Pred. No. 96;
	Matches 39; Conservative 26; Mismatches 77; Indels 51; Gaps 7;	
Qy	41 PCQAQQWEGRVNMVQOSSGSRNALL-----SYDGLNQVRVLDERKALIPCKRL	91
Dd	82 PVQMMLWP-RMALENLSGEDYFLREKNLDGSIHYSLOSWLRTVEERRMM--ERG	138
Qy	92 FEYLILYKGVMFOIDATQCSKWLTLPQWDPILDIFQNSTFEDQYSIGQGEOITVOEW	151
Dd	139 F-----LPPQQRKDFFDLCSLPDLNKETLENL	166
Qy	152 SDRKSARSYETWIG-IYTVKDCYPVQETFNTINYSVILTSTRFD-IQLGIKDPSVFPTPST	209
Dd	167 RDRFKHEKIYYVGSIILIVNPFFELIYNPKY-----VKMYDNHQLGKPEPHIYAADV	221
Qy	210 CQMAQLEKMSEDCC	222
Dd	222 AYHAMLRKKNOQC	234

Search completed: June 10, 2006, 02:57:39
Job time : 46 secs

OM protein - protein search, using sw model

Run on: June 10, 2006, 02:48:39 ; Search time 296 seconds
(without alignments)
700.012 Million cell updates/sec

Title: US-10-733-646-2
Perfect score: 1214
Sequence: 1 MFCGRAPLRTVPGALGAWLLG.....TPPSTCQMAQLKMSDSCSW 224

Scoring table: BLOSUM62

Gapop.10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1214	100.0	224	1 EPDR1_HUMAN	Q9um22 homo sapien
2	1206	99.3	344	2 Q96J80_HUMAN	Q96J80 homo sapien
3	1194	98.4	224	2 Q99M77_MOUSE	Q99M77 mus musculus
4	1168	96.2	227	2 Q95K54_MACPA	Q95K54 macaca fasc
5	1164	95.9	224	1 EPDR1_MACPA	Q9n0c7 macaca fasc
6	1164	95.9	227	2 Q95K77_MACPA	Q95K77 macaca fasc
7	1102.5	90.8	218	2 Q95K56_MACPA	Q95K56 macaca fasc
8	1000	82.4	224	2 Q99W71_MOUSE	Q99W71 m mammalian
9	994	81.9	224	2 Q8CA12_MOUSE	Q8CA12 mus musculus
10	993	81.8	224	2 Q5X110_RAT	Q5X110 rattus norv
11	986	81.2	224	2 Q8BQ11_MOUSE	Q8BQ11 mus musculus
12	683.5	56.3	206	2 Q6DH25_BRARE	Q6dh25 brachydanio
13	434.5	35.8	234	2 Q6EBF4_9ECHN	Q6eef4 holothuria
14	288	23.7	194	2 Q61WN5_BRABE	Q61wn5 branchiosto
15	192.5	15.9	221	1 EPD2_ONCMY	P28771 oncorhynch
16	192	15.8	211	2 Q4TFW4_TETNG	Q4tfw4 tetraodon n
17	190.5	15.7	221	1 EPD1_ONCMY	P28770 oncorhynch
18	189.5	15.6	221	1 EPD2_SALSA	P28772 salmo salar
19	185.5	15.3	221	1 EPD_ESOLI	P32188 esox lucius
20	181	14.9	181	2 Q90394_9TELE	Q90394 chalcinus sp
21	177	14.6	178	2 Q91083_9TELE	Q91083 leporinus s
22	174.5	14.4	178	2 Q91140_9TELE	Q91140 nanobrycon
23	173	14.3	178	2 Q91253_9TELE	Q91253 phenacogram
24	173	14.3	181	2 Q91109_9TELE	Q91109 metynnis sp
25	172	14.2	178	2 Q91052_9TELE	Q91052 gymnocorymb
26	167.5	13.8	215	1 EPD_CYPEA	P38528 cyprinus ca
27	164.5	13.6	183	2 Q90492_9TELE	Q90492 distichodus
28	163.5	13.5	212	1 EPD_CLUHA	P32187 clupea hare
29	159	13.1	218	1 EPD_DANAE	Q90399 danio aequi
30	158	13.0	214	1 EPD_NOTCH	Q91130 notropis ch
31	157.5	13.0	216	2 Q4S8U8_TETNG	Q4s8u8 tetraodon n

32 156.5 12.9 215 1 EPD1_CARAU

33 154.5 12.7 217 1 EPD_BRARE

34 154 12.7 180 2 Q91331_9TELE

35 153.5 12.6 215 1 EPD2_CARAU

36 152.5 12.6 186 2 Q91465_9TELE

37 148 12.2 170 2 Q90241_9TELE

38 147.5 12.1 136 2 Q91254_9TELE

39 146 12.0 172 2 Q91057_9TELE

40 132.5 10.9 140 2 Q91045_9TELE

41 131 10.8 203 2 Q6WNG6_BRABE

42 129.5 10.7 131 2 Q90276_9TELE

43 125.5 10.3 137 2 Q91056_9TELE

44 125 10.3 192 2 Q91464_9TELE

45 123 10.1 133 2 Q91059_9TELE

ALIGNMENTS

RESULT 1

EPDR1_HUMAN STANDARD; PRT; 224 AA.

AC Q9UM22; 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.

DT 21-FEB-2001, sequence version 2.

DT 07-FEB-2006, entry version 40.

DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).

DE Protein).

GN Name=EPDR1; Synonyms=MERP1, UCC1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21622606; PubMed=11749721; DOI=10.1093/10454901753340613; RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M., Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.; "Identification and characterization of a novel family of mammalian ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic, and malignant tissues.";

RT DNA Cell Biol. 20:625-635(2001).

RL [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Cervix;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RN [3]

RP NUCLEOTIDE SEQUENCE OF 51-224.

RA Niamrich I., Erdmann S., Melchers U.;

RT "Genes that are differentially expressed in colon cancer.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Secreted protein.


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Db 1 MFGRAPLRTVPGALGFWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
|||
61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
|||
61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 120
|||
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQEWSDRSARSYETWIGIYTKDCYPVOETFT 180
121 PWDPLDIPONSTFEDQYSIGGPOEQIMVQEWSDRSARSYETWIGIYTKDCYPVOETFT 180
181 INYSVILSTRFRFDIOLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
181 KNYSVILSTRFRFDIOLGKIDPSVFTPPSTCQIAQLEKMSDCSW 224
```

```
RESULT 6
Q95K77 MACFA PRELIMINARY; PRT; 227 AA.
AC Q95K77;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Temporal lobe right;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
RA Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT chromosomes.";
RL Gene 275:31-37(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AB063094; BAB60800.1; -; mRNA.
DR EMBL; AB097520; BAC41745.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25821 MW; BE6A77C5867DA50A CRC64;
Query Match 95.9%; Score 1164; DB 2; Length 227;
Best Local Similarity 96.0%; Pred. No. 5.3e-102;
Matches 215; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 MFGRAPLRTVPGALGFWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
Db 4 MFGRAPLRTVPGALGFWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 63
|||
61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
|||
64 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 123
|||
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQEWSDRSARSYETWIGIYTKDCYPVOETFT 180
124 PWDPLDIPONSTFEDQYSIGGPOEQIMVQEWSDRSARSYETWIGIYTKDCYPVOETFT 183
181 INYSVILSTRFRFDIOLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
184 KNYSVILSTRFRFDIOLGKIDPSVFTPPSTCQIAQLEKMSDCSW 227

RESULT 7
Q95K56 MACFA PRELIMINARY; PRT; 218 AA.
AC Q95K56;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; AB066535; BAB62211.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24970 MW; 8B8524C0D986677C CRC64;
```

```
Query Match 90.8%; Score 1102.5; DB 2; Length 218;
Best Local Similarity 92.0%; Pred. No. 3.5e-96;
Matches 206; Conservative 4; Mismatches 5; Indels 9; Gaps 1;

QY 1 MFGRAPLRTVPGALGFWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 60
Db 4 MFGRAPLRTVPGALGFWLLGCLWAWTLGCLSLGAVGAPRPCOAPQOWEGRWYQOQSSG 54
|||
61 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
|||
55 RNSRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKDGVMFQIEQATKQCSKMTLT 114
|||
121 PWDPLDIPONSTFEDQYSIGGPOEQITVQEWSDRSARSYETWIGIYTKDCYPVOETFT 180
115 PWDPLDIPONSTFEDQYSIGGPOEQIMVQEWSDRSARSYETWIGIYTKDCYPVOETFT 174
181 INYSVILSTRFRFDIOLGKIDPSVFTPPSTCQMAQLEKMSDCSW 224
```


Db 175 KNYSVILSTRFFDTQLGKIDPSVFTPBTPCQIAQLEKMSDCSW 218

RESULT 8

ID Q99M71_MOUSE PRELIMINARY; PRT; 224 AA.
AC Q99M71;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 29.
DE Mammalian ependymin related protein-2 (Ependymin 2) (Adult male
DE diencephalon cDNA, RIKEN full-length enriched library,
DE clone:9330154O03 product:mammalian ependymin related protein-2) (Adult
DE male cerebellum cDNA, RIKEN full-length enriched library,
DE clone:1500034M21 product:Mammalian ependymin related protein-2
DE (Similar to mammalian ependymin related protein 1), full insert
DE sequence).
GN Name=Epd2; Synonyms=AU040950, MERP2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J and C57BL/6J;
RX MEDLINE=21622606; PubMed=1749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635 (2001).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares T.B., Tonhyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Kidney;
RC Director MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Balla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Wiki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
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RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
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RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=21085660; PubMed=111217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Iehli Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Iehli Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
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RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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DB 181 RNYTVMSRFRFDVQLGINKDPVSFTPTPSTCQAAQPEKMSDGS 223
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AC 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
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DE clone:A230058H08 product:MAMMALIAN EPENDYMIN RELATED PROTEIN-2
DE (SIMILAR TO MAMMALIAN EPENDYMIN RELATED PROTEIN 1) homolog.
GN Name=EpdR2; Synonyms=AU040950;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX PubMed=16141072; DOI=10.1136/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A.,
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RA Baisak M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
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RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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RA Mattagui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
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RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
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RA Yamashiki H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brueic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kohjima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
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GenCore version 5.1.9
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-09-229-583A-2
; Sequence 2, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
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US-09-229-583A-2

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RESULT 2
US-09-242-890-11
; Sequence 11, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro

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; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 11
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; TYPE: PRT
; ORGANISM: Human
; US-09-242-890-11

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; Patent No. 6683161
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; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: Pf403D1
; CURRENT APPLICATION NUMBER: US/10/187,904
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
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Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSG 60
```

```
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
Db 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
Db 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
Db 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224

RESULT 4
US-09-242-890-10
; Sequence 10, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Human
; US-09-242-890-10

Query Match      89.0%; Score 1081; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKA 84
Db 1 WTLGCLSLGAVGAPRCPQAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQ 144
Db 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQ 120
QY 145 QITVQWSDRKSARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 204
Db 121 QITVQWSDRKSARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 180
QY 205 TTPSTCQMAQLEKMSDCSW 224
Db 181 TTPSTCQMAQLEKMSDCSW 200

RESULT 5
US-09-242-890-1
; Sequence 1, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
```

; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-1

Query Match 82.8%; Score 1005; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.8e-108;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 APPRCPAQQWEGQVQVQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEVILL 97
DB 1 APPRCPAQQWEGQVQVQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEVILL 60
QY 98 YKDGVMFQIDQATKQCSKMTLTQPDLPONSTFEDQYSIGGPOEITVQWSDRKS 157
DB 61 YKDGVMFQIDQATKQCSKMTLTQPDLPONSTFEDQYSIGGPOEITVQWSDRKS 120
QY 158 RSYETWIGIVTKDCYVQVQTFITINYSVILSTRFFDIQIGKIDPSVFTPPSTCMAQLEK 217
DB 121 RSYETWIGIVTKDCYVQVQTFITINYSVILSTRFFDIQIGKIDPSVFTPPSTCMAQLEK 180
QY 218 MSEDCSW 224
DB 181 MSEDCSW 187

RESULT 6
US-09-242-890-13
; Sequence 13, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 13
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-13

Query Match 82.4%; Score 1000; DB 2; Length 224;
Best Local Similarity 80.3%; Pred. No. 8.9e-108;
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;
QY 1 MPCRPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPAQQWEGQVQVQSSG 60
DB 1 MPAPARRLVQGRGTWLLGSLVWVLCGLMGAGSLGTPOPCAPQWEGQVLYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

DB 61 HNNRALVSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCAKIPLVE 120
QY 121 PWDPLDIPONSTFEDQYSIGGPOEITVQWSDRKSARSYETWIGIVTKDCYVQVQTFIT 180
DB 121 SWDPLDIPONSTFEDQYSIGGPOEITVQWSDRKSARSYETWIGIVTKDCYVQVQTFIT 180
QY 181 INYSVILSTRFFDIQIGKIDPSVFTPPSTCMAQLEKMSDSCS 223
DB 181 RNYTVVMSTRFFDVQLGIDKIDPSVFTPPSTCMAQLEKMSDSCS 223

RESULT 7
US-09-242-890-12
; Sequence 12, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-12

Query Match 81.8%; Score 993; DB 2; Length 224;
Best Local Similarity 81.8%; Pred. No. 5.8e-107;
Matches 180; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
QY 4 RAPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRCPAQQWEGQVQVQSSGRNS 63
DB 4 RAPRLVQGPRETWLLGGLWVWLCGLMGAGSPGTPOPCAPQWEGQVLYQSSGHS 63
QY 64 RALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPD 123
DB 64 RALVSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCAKIPLAE 123
QY 124 PLDIPONSTFEDQYSIGGPOEITVQWSDRKSARSYETWIGIVTKDCYVQVQTFIT 183
DB 124 PLDIPONSTFEDQYSIGGPOEITVQWSDRKSARSYETWIGIVTKDCYVQVQTFIT 183
QY 184 SVILSTRFFDIQIGKIDPSVFTPPSTCMAQLEKMSDSCS 223
DB 184 TVVLSTRFFDVQLGIDKIDPSVFTPPSTCMAQLEKMSDSCS 223

RESULT 8
US-09-242-890-2
; Sequence 2, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10

; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-2

Query Match 73.5%; Score 892; DB 2; Length 190;
Best Local Similarity 86.1%; Pred. No. 2.5e-95;
Matches 161; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 37 GAPPQAPQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 96
Db 3 GTPQCPAQWEGRQVLYQSSGHNRRALVSVDGLNQRVRLDERKALIPCKRLFYIL 62

QY 97 LYKGVWFQIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQYSIGGPGQEQITVQEWSDRKS 156
Db 63 LYKGVWFQIEQATKCAKIPAEHPDPLDIPQNSTFFEDQYSIGGPGQEQIMVQWNSDRRT 122

QY 157 ARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQLE 216
Db 123 ARSYETWIGYTVKDCYPVQETFTIRNVTYVLSSTRFFDVQLGKDPSPVFTPPSTCQTAQPE 182

QY 217 KMSDCS 223
Db 183 KMKENS 189

RESULT 9
US-09-242-890-3
; Sequence 3, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-3

Query Match 72.1%; Score 875; DB 2; Length 187;
Best Local Similarity 84.9%; Pred. No. 2.3e-93;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 39 PRECPAQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYIL 98
Db 2 POPCPAQWEGRQVLYQSSGHNRRALVSVDGLNQRVRLDERKALIPCKRLFYIL 61

QY 99 KGVWFQIDQATKQCSKMTLTQPDPLDIPQNSTFFEDQYSIGGPGQEQITVQEWSDRKSAR 158
Db 62 KGVWFQIEQATKCAKIPLVESWDPLDIPQNSTFFEDQYSIGGPGQEQILVQWNSDRRTAR 121

QY 159 SYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVFTPPSTCQMAQLEKM 218
Db 122 SYETWIGYTVKDCYPVQETFTIRNVTYVLSSTRFFDVQLGKDPSPVFTPPSTCQAAQPEKM 181

QY 219 SEDCS 223
Db 182 SDGCS 186

RESULT 10
US-09-242-890-14
; Sequence 14, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-14

Query Match 17.2%; Score 209; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVG 37
Db 1 MFGRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVG 37

RESULT 11
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like

US-09-242-890-8

Query Match 16.6%; Score 201; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.4e-16;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 SYDGLNQRVRLDERKALIPCKRLFEYLLYKDGWMFQI 106
Db 1 SYDGLNQRVRLDERKALIPCKRLFEYLLYKDGWMFQI 39

RESULT 12

US-09-229-583A-4
; Sequence 4, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncoerhynchus mykiss
US-09-229-583A-4

Query Match 15.9%; Score 192.5; DB 2; Length 221;
Best Local Similarity 25.0%; Pred. No. 7.8e-14;
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

Qy 25 WTLGCLSLGAVGAPRCQAPQOQWEGRQVMYQSSGSRALLSYDGLNQRVRLDERKA 84
Db 12 WLCGATALAESHGPHOCHTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRTSEMH 71
Qy 85 LIPCKRLFEYLLYKDGWMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFFEDQYSIGG--- 141
Db 72 LNKTEHLEDYLMLEEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV 131
Qy 142 PQEQITVQWSDRSARSYETWIGIYTVKDCYPQVETFTINYSVILSTRFPDIQLGKDP 201
Db 132 QEDNIKVINWVG-SVAETKQYSALTTVGECPL-STFYSTDSTITLLFSNSVTVTKAP 189

Qy 202 SVETPSTCQMAQLEK 217

Db 190 EMFTLPSFCEAVELEE 205

RESULT 13

US-10-187-904-4
; Sequence 4, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D1
; CURRENT APPLICATION NUMBER: US/10/187,904
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

; LENGTH: 221

; TYPE: PRT

; ORGANISM: Oncoerhynchus mykiss

US-10-187-904-4

Query Match 15.9%; Score 192.5; DB 2; Length 221;
Best Local Similarity 25.0%; Pred. No. 7.8e-14;
Matches 49; Conservative 39; Mismatches 103; Indels 5; Gaps 3;

Qy 25 WTLGCLSLGAVGAPRCQAPQOQWEGRQVMYQSSGSRALLSYDGLNQRVRLDERKA 84
Db 12 WLCGATALAESHGPHOCHTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRTSEMH 71
Qy 85 LIPCKRLFEYLLYKDGWMFQIDQATKQCSKMTLTQPWDPLDIPQNSTFFEDQYSIGG--- 141
Db 72 LNKTEHLEDYLMLEEGVFYDIDMKQSCCKMSLHSHAHLELPAGAHHQVELFLGSDTV 131
Qy 142 PQEQITVQWSDRSARSYETWIGIYTVKDCYPQVETFTINYSVILSTRFPDIQLGKDP 201
Db 132 QEDNIKVINWVG-SVAETKQYSALTTVGECPL-STFYSTDSTITLLFSNSVTVTKAP 189
Qy 202 SVETPSTCQMAQLEK 217
Db 190 EMFTLPSFCEAVELEE 205

RESULT 14

US-09-242-890-5
; Sequence 5, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependymin
US-09-242-890-5

Query Match 14.4%; Score 175; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.2e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 QIDQATKQCSKMTLTQPWDPLDIPQNSTFFEDQ 136
Db 1 QIDQATKQCSKMTLTQPWDPLDIPQNSTFFEDQ 32

RESULT 15

US-09-229-583A-5
; Sequence 5, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A

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; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Cyprinus carpio
; US-09-229-583A-5

Query Match      13.8%; Score 167.5; DB 2; Length 215;
Best Local Similarity 24.4%; Pred. No. 6e-11;
Matches 50; Conservative 47; Mismatches 89; Indels 19; Gaps 8;

Qy   30 LCSLGAVGAPR-PCQAPQWEGRQVMYQSSGRNSRAL--LSYDGLNQRVRLDERKALI 86
Db   14 LCVAWASSNRQPCCHSPPLTSG--TMKWSTGGHDLASGEFSYDSKANKRFVEDTAHAN 71
Qy   87 PCKRLFEYILLYKGYVMFQIDQATKQCSKMTLTQPWDPLDIPONSTFDQYSIGGP---Q 143
Db   72 KTSHM-DVLVHPREGVLYEIDSKNESCKKETLQFRKHLMEIPPDATHESEIYMGSPSITE 130
Qy   144 EQITVOEWSDR----KSARSYETWIGIYTKDCYPVQETETINYSVILSTRFPDIOLGIK 199
Db   131 QGLRVRVWNGKLPDLHAHYSLSL-----TSCGCLPVSGSYGDKDLLFS-FFGVETEVD 184
Qy   200 DPSVFTPPSTCQMAQLEKMSDCSW 224
Db   185 DPQVFVPPAYCEAVAFEEAPDDHSF 209
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Search completed: June 10, 2006, 02:58:31
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 10, 2006, 02:57:54 ; Search time 185 Seconds
(without alignments)
560.866 Million cell updates/sec

Title: US-10-733-646-2
Perfect score: 1214
Sequence: 1 MPRAPLRTVPGALGAWLLG.....TPPSTCQMAQLEKMSDCSW 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1214	100.0	224	4	US-10-612-788-11
2	1214	100.0	224	4	US-10-733-646-2
3	1214	100.0	224	5	US-10-733-646-2
4	1081	89.0	200	4	US-10-612-788-10
5	1005	82.8	187	4	US-10-612-788-1
6	1000	82.4	224	4	US-10-612-788-13
7	993	81.8	224	4	US-10-612-788-12
8	892	73.5	190	4	US-10-612-788-2
9	875	72.1	187	4	US-10-612-788-3
10	209	17.2	37	4	US-10-612-788-14
11	201	16.6	39	4	US-10-612-788-8
12	192.5	15.9	221	4	US-10-733-646-4
13	192.5	15.9	221	5	US-10-733-646-4
14	175	14.4	32	4	US-10-612-788-5
15	167.5	13.8	215	4	US-10-733-646-5
16	167.5	13.8	215	5	US-10-733-646-5
17	163.5	13.5	212	4	US-10-733-646-7
18	163.5	13.5	212	5	US-10-733-646-7
19	154.5	12.7	217	4	US-10-733-646-6
20	154.5	12.7	217	5	US-10-733-646-6
21	153.5	12.6	216	4	US-10-733-646-3
22	153.5	12.6	216	5	US-10-733-646-3
23	147	12.1	26	4	US-10-612-788-9
24	143	11.8	25	4	US-10-612-788-6
25	133	11.0	24	4	US-10-612-788-15
26	125	10.3	37	4	US-10-612-788-17
27	102	8.4	34	4	US-10-612-788-16

Sequence 7, Appli
Sequence 32, Appli
Sequence 34, Appli
Sequence 32, Appli
Sequence 34, Appli
Sequence 39, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 162, App
Sequence 98, Appli
Sequence 5096, Ap
Sequence 2652, Ap
Sequence 2989, Ap
Sequence 135, App
Sequence 120, App
Sequence 61631, A
Sequence 1811, Ap

28 7.7 17 4 US-10-612-788-7
29 6.8 338 3 US-09-880-505-32
30 6.8 338 3 US-09-880-505-34
31 6.8 338 4 US-10-051-643-32
32 6.8 338 4 US-10-051-643-34
33 6.8 338 4 US-10-329-087-39
34 6.8 338 4 US-10-203-562-4
35 6.8 338 4 US-10-332-512A-1
36 6.8 338 5 US-10-695-155-162
37 6.8 133 4 US-10-612-665-98
38 6.8 193 4 US-10-676-694-98
39 6.8 419 4 US-10-724-972A-5096
40 6.7 758 4 US-10-408-765A-2652
41 6.7 830 4 US-10-408-765A-2989
42 6.7 970 4 US-10-351-157-135
43 6.7 970 4 US-10-352-554-120
44 6.7 10421 4 US-10-282-122A-61631
45 6.6 896 4 US-10-408-765A-1811

ALIGNMENTS

RESULT 1
US-10-612-788-11
; Sequence 11, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417U51P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: human
US-10-612-788-11

Query Match 100.0%; Score 1214; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRPPCOAPQOQWEGQVMYQSSG 60
Db 1 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRPPCOAPQOQWEGQVMYQSSG 60
Qy 61 RNSRALLSYDGLNQRVRLDERKALIPCKELFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
Db 61 RNSRALLSYDGLNQRVRLDERKALIPCKELFEYLLYKDGVMFQIDQATKQCSKMTLTQ 120
Qy 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180
Db 121 PWDPLDIPQNSTFEDQYISGPGQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180
Qy 181 INYSVILSTFRFFDIQIGIKDPSVFTTPTSTCMAQLEKMSDCSW 224
Db 181 INYSVILSTFRFFDIQIGIKDPSVFTTPTSTCMAQLEKMSDCSW 224

RESULT 2
US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.

```
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1214; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||

QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||
Db 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
Db 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
Db 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||
Db 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||

Query Match      100.0%; Score 1214; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||

QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||
Db 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
Db 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||
Db 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||

RESULT 3
US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1214; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6e-117;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||
```

```
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSG 60
    |||
QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||
Db 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
    |||

QY 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||
Db 121 PWDPLDIPONSTPEDQYSIGGPQEQITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFT 180
    |||

QY 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||
Db 181 INYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKMSDCSW 224
    |||

RESULT 4
US-10-612-788-10
; Sequence 10, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1p
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: human
US-10-612-788-10

Query Match      89.0%; Score 1081; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 1.9e-103;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSGRNALLSYDGLNQRVRVLDERKA 84
    |||
Db 1 WTLGGLCSLGAVGAPRCPQAPQWEGROVMYQOSSGRNALLSYDGLNQRVRVLDERKA 60
    |||

QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTPEDQYSIGGPQE 144
    |||
Db 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTPEDQYSIGGPQE 120
    |||

QY 145 QITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTINYSVILSTRFFDIQLGIKDPVSF 204
    |||
Db 121 QITVOEWSDRKSARSYETWIGIYTVKDCYPVOETFTINYSVILSTRFFDIQLGIKDPVSF 180
    |||

QY 205 TPPSTCQMAQLEKMSDCSW 224
    |||
Db 181 TPPSTCQMAQLEKMSDCSW 200
    |||

RESULT 5
US-10-612-788-1
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1p
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
```


;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1
;; LENGTH: 187
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-612-788-1

Query Match 82.8%; Score 1005; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.3e-95;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 APPPCAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
DB 1 APPPCAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
QY 98 YKGVNMFQIDQATKQCSKMTLTQWDPDLPQNSTFEDQYSIGGPEQITVQWSDRKS 157
DB 61 YKGVNMFQIDQATKQCSKMTLTQWDPDLPQNSTFEDQYSIGGPEQITVQWSDRKS 120
QY 158 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIOLGIKDPVSFTTPTSTCMAQLEK 217
DB 121 RSYETWIGYTVKDCYVQETFTINYSVILSTRFFDIOLGIKDPVSFTTPTSTCMAQLEK 180
QY 218 MSEDCSW 224
DB 181 MSEDCSW 187

RESULT 6

US-10-612-788-13
;; Sequence 13, Application US/10612788
;; Publication No. US20040014947A1
;; GENERAL INFORMATION:
;; APPLICANT: ONDA, Haruo
;; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
;; FILE REFERENCE: 2417USIP
;; CURRENT APPLICATION NUMBER: US/10/612,788
;; CURRENT FILING DATE: 2003-07-02
;; PRIOR APPLICATION NUMBER: 09/242,890
;; PRIOR FILING DATE: 1999-02-25
;; PRIOR APPLICATION NUMBER: PCT/JP97/03194
;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 13
;; LENGTH: 224
;; TYPE: PRT
;; ORGANISM: Mouse
US-10-612-788-13

Query Match 82.4%; Score 1000; DB 4; Length 224;
Best Local Similarity 80.3%; Pred. No. 5.6e-95;
Matches 179; Conservative 19; Mismatches 25; Indels 0; Gaps 0;
QY 1 MPCRRLTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRPPQAPQWEGRQVMYQSSG 60
DB 1 MPARAPRLVQGPRTWLLGSLWVWLGLMGAGSLGTTPQCPAQWEGRQVLYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQIDQATKQCSKMTLTQ 120
DB 61 HNNRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQIDQATKQCAKPLVE 120
QY 121 PWDPLDPQNSTFEDQYSIGGPEQILVQWSDRKSARSYETWIGYTVKDCYVQETFT 180
DB 121 SMDPLDPQNSTFEDQYSIGGPEQILVQWSDRKSARSYETWIGYTVKDCYVQETFT 180
QY 181 INYSVILSTRFFDIOLGIKDPVSFTTPTSTCMAQLEKMSDSCS 223
DB 181 RNYTVVMSTRFFDVQLGIKDPVSFTTPTSTCMAQPEKMSDSCS 223

RESULT 7

US-10-612-788-12
;; Sequence 12, Application US/10612788
;; Publication No. US20040014947A1
;; GENERAL INFORMATION:
;; APPLICANT: OGI, Kazuhiro
;; APPLICANT: ONDA, Haruo
;; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
;; FILE REFERENCE: 2417USIP
;; CURRENT APPLICATION NUMBER: US/10/612,788
;; CURRENT FILING DATE: 2003-07-02
;; PRIOR APPLICATION NUMBER: 09/242,890
;; PRIOR FILING DATE: 1999-02-25
;; PRIOR APPLICATION NUMBER: PCT/JP97/03194
;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 12
;; LENGTH: 224
;; TYPE: PRT
;; ORGANISM: Rat
US-10-612-788-12

Query Match 81.8%; Score 993; DB 4; Length 224;
Best Local Similarity 81.8%; Pred. No. 3e-94;
Matches 180; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
QY 4 RAPLRTVPGALGAWLLGGLWMTLCGLCSLGAVGAPRPPQAPQWEGRQVMYQSSGRNS 63
DB 4 RAPRRLVQGPRTWLLGSLWVWLGLMGAGSLGTTPQCPAQWEGRQVLYQSSGHNS 63
QY 64 RALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQIDQATKQCSKMTLTQWPD 123
DB 64 RALVSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQIDQATKCAKPLAEFPD 123
QY 124 PLDIPQNSTFEDQYSIGGPEQITVQWSDRKSARSYETWIGYTVKDCYVQETFTINY 183
DB 124 PLDIPQNSTFEDQYSIGGPEQILVQWSDRKSARSYETWIGYTVKDCYVQETFTIRNY 183
QY 184 SVILSTRFFDIOLGIKDPVSFTTPTSTCMAQLEKMSDSCS 223
DB 184 TVVLSTRFFDVQLGIKDPVSFTTPTSTCQTAQPEKMKENCS 223

RESULT 8

US-10-612-788-2
;; Sequence 2, Application US/10612788
;; Publication No. US20040014947A1
;; GENERAL INFORMATION:
;; APPLICANT: OGI, Kazuhiro
;; APPLICANT: ONDA, Haruo
;; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
;; FILE REFERENCE: 2417USIP
;; CURRENT APPLICATION NUMBER: US/10/612,788
;; CURRENT FILING DATE: 2003-07-02
;; PRIOR APPLICATION NUMBER: 09/242,890
;; PRIOR FILING DATE: 1999-02-25
;; PRIOR APPLICATION NUMBER: PCT/JP97/03194
;; PRIOR FILING DATE: 1997-09-10
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2
;; LENGTH: 190
;; TYPE: PRT
;; ORGANISM: Rat
US-10-612-788-2

Query Match 73.5%; Score 892; DB 4; Length 190;
Best Local Similarity 86.1%; Pred. No. 7.1e-84;
Matches 161; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
QY 37 GAPRPCAPQWEGRQVMYQSSGRNALLSYDGLNQRVRLDERKALIPCKRLFEYIL 96

Db 3 GTPQCPAQWEGRQVLQQSSGHNRAVSDGLNQVRVLDERKALIPCKRLFYIL 62
QY 97 LYKDGVMFQIDQATKQCSKMTLTQPDPLDPQNSTFEDQYSIGGPQEQITVQWSDRKS 156
Db 63 LYKDGVMFQIEQATKCAKIPAEPLDIPQNSTFEDQYSIGGPQEQIMVQWSDRRT 122
QY 157 ARSYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLE 216
Db 123 ARSYETWIGYTAADKCPVQETFIRNYTVVLSTRFFDVQLGDKDPSVFTPPSTCQTAQPE 182
QY 217 KMSDCS 223
Db 183 KMKENS 189

RESULT 9
US-10-612-788-3
; Sequence 3, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: mouse
US-10-612-788-3

Query Match 72.1%; Score 875; DB 4; Length 187;
Best Local Similarity 84.9%; Pred. No. 4e-82;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
QY 39 PRPCAPQWEGRQVWYQSSGHNRAVSDGLNQVRVLDERKALIPCKRLFYILLY 98
Db 2 POPCPAQWEGRQVLYQSSGHNRAVSDGLNQVRVLDERKALIPCKRLFYILLY 61
QY 99 KDGVMFQIDQATKQCSKMTLTQPDPLDPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 158
Db 62 KEGVMFQIEQATKQCAKIPVSWDPLDIPQNSTFEDQYSIGGPQEQILVQWSDRTAR 121
QY 159 SYETWIGYTVKDCYPVQETFTINYSVILSTRFFDIQIGIKDPSVFTPPSTCQMAQLEKX 218
Db 122 SYETWIGYTVKDCYPVQETFTIRNYTVVWSTRFFDVQLGDKDPSVFTPPSTCQAAQPEKX 181
QY 219 SEDCS 223
Db 182 SDGCS 186

RESULT 10
US-10-612-788-14
; Sequence 14, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: human
US-10-612-788-14
Query Match 17.2%; Score 209; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVG 37
Db 1 MPGRAPLRTVPGALGAWLLGGLWAWTLCGLCSLGAVG 37
RESULT 11
US-10-612-788-8
; Sequence 8, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-8
Query Match 16.6%; Score 201; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 106
Db 1 SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 39

RESULT 12
US-10-733-646-4
; Sequence 4, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221

Qy 200 DPSVFTTPTCQMAQLEKMSDCSW 224
Db 185 DPQVFPAYCEAVAFEEAPDDHSF 209

Search completed: June 10, 2006, 03:01:42
Job time : 186 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 10, 2006, 02:58:49 ; Search time 16 Seconds
(without alignments)
177.005 Million cell updates/sec

Title: US-10-733-646-2
Perfect score: 1214
Sequence: 1 MPCRAPLRTVPGALWLLG.....TPPSTCOMAQLKMSDCSW 224

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pdb:
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pdb:
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pdb:
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pdb:
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pdb:
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pdb:
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pdb:
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pdb:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	7.2	931	6	US-10-524-979-2
2	75.5	6.2	164	7	US-11-293-697-2800
3	74	6.1	1456	6	US-10-505-928-69
4	72.5	6.0	790	7	US-11-318-939-13
5	69.5	5.7	413	6	US-10-953-349-24222
6	69.5	5.7	429	6	US-10-953-349-24221
7	69.5	5.7	431	6	US-10-953-349-24220
8	69.5	5.7	3882	6	US-10-953-349-5549
9	69.5	5.7	3978	6	US-10-953-349-5548
10	69.5	5.7	4118	6	US-10-953-349-5547
11	69	5.7	193	7	US-11-183-218-16
12	69	5.7	802	7	US-11-293-697-3610
13	67.5	5.6	294	6	US-10-953-349-5105
14	67.5	5.6	383	6	US-10-953-349-5104
15	67.5	5.6	439	6	US-10-953-349-5103
16	67.5	5.6	585	7	US-11-233-697-4164
17	66	5.4	184	6	US-10-953-349-28907
18	66	5.4	208	6	US-10-953-349-28906
19	66	5.4	272	6	US-10-953-349-28905
20	66	5.4	730	6	US-10-505-928-841
21	65.5	5.4	371	6	US-10-953-349-11789
22	65.5	5.4	404	6	US-10-953-349-11788
23	65.5	5.4	409	6	US-10-953-349-11787
24	65.5	5.4	1871	6	US-10-501-834-26
25	65	5.4	695	7	US-11-293-697-4190

26	64.5	5.3	911	7	US-11-313-450-25	Sequence 25, Appl
27	64	5.3	111	6	US-10-953-349-30150	Sequence 30150, A
28	64	5.3	274	7	US-11-293-697-4076	Sequence 4076, Ap
29	64	5.3	362	7	US-11-293-697-2645	Sequence 2645, Ap
30	63.5	5.2	333	6	US-10-953-349-28481	Sequence 28481, A
31	63.5	5.2	337	6	US-10-953-349-28480	Sequence 28480, A
32	63.5	5.2	345	6	US-10-953-349-28479	Sequence 28479, A
33	63.5	5.2	453	6	US-10-471-571A-1056	Sequence 1056, Ap
34	63.5	5.2	524	7	US-11-293-697-3442	Sequence 3442, Ap
35	63	5.2	174	6	US-10-953-349-4320	Sequence 4320, Ap
36	63	5.2	201	6	US-10-196-749-108	Sequence 108, App
37	63	5.2	277	6	US-10-953-349-4319	Sequence 4319, Ap
38	63	5.2	286	6	US-10-953-349-4318	Sequence 4318, Ap
39	63	5.2	639	7	US-11-293-697-3425	Sequence 3425, Ap
40	63	5.2	847	6	US-10-505-928-495	Sequence 495, App
41	62.5	5.1	208	6	US-10-953-349-30987	Sequence 30987, A
42	62.5	5.1	244	6	US-10-953-349-30986	Sequence 30986, A
43	62.5	5.1	293	6	US-10-953-349-19396	Sequence 19396, A
44	62.5	5.1	324	6	US-10-953-349-19395	Sequence 19395, A
45	62.5	5.1	359	6	US-10-953-349-19394	Sequence 19394, A

ALIGNMENTS

RESULT 1
US-10-524-979-2
; Sequence 2, Application US/10524979
; Publication No. US20060094013A1
; GENERAL INFORMATION:
; APPLICANT: Takemori, Hiroshi
; APPLICANT: Okamoto, Mitsuhiko
; TITLE OF INVENTION: SALT-INDUCIBLE KINASE 2 AND USE THEREOF
; FILE REFERENCE: WATA-003
; CURRENT APPLICATION NUMBER: US/10/524,979
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 2002-240092
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 2003-23295
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-524-979-2

Query Match	7.2%	Score 88;	DB 6;	Length 931;
Best Local Similarity	23.3%	Pred. No. 0.38;		
Matches	59;	Conservative	34;	Mismatches 80; Indels 80; Gaps 15;
Qy	37	GAPRCPQAPQWEGRQ	-----VNYQSSGNSRALLSYDG-----LNQVRV 78	
Db	178	GSP-PYAAPEVFEGQYEGPQLDIWSMGVLYLVLCG-----ALPFDGPTLPILRQRYL- 230		
Qy	79	LDERKALIP-----CKRLFYILLYKDGVMFQIDQATKOCCKMTLTQPWD-PLDIPONS 131		
Db	231	--EGRFPIPYFMEDCEHLIRMLDLDPKRLSLAQ-IKEHKWMLIEVPVORPILYPOEQ 287		
Qy	132	TFEDQYSIGGPQEQ-----ITVQWSDRSARSYETWIGIYTV-----KDCYP 174		
Db	288	--ENEPSIGFNEQVLRMLHSLGIDQKTVESLQNKSNYHFAIYFLLVERLKHRSRFP 345		
Qy	175	VQETP-----TINYSVILSTRFFDIQIGIKDPSV-----FT-PPST 209		
Db	346	VEQRLDGRQRPSTIAEQTVAKAQTVGLPVLTHPPNRLMRSTLLPOASNVEAFSFTSS 405		
Qy	210	COMAQLEKMSDC 222		
Db	406	CQ-AEAFMBEEC 417		

```
RESULT 2
US-11-293-697-2800
; Sequence 2800, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2800
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2800

Query Match          6.2%; Score 75.5; DB 7; Length 164;
Best Local Similarity 37.7%; Pred. No. 0.83;
Matches 20; Conservative 5; Mismatches 27; Indels 1; Gaps 1;

QY  5  APLRTVPGALGAWLLGGLWNTLCGLC-SLGAVGAPRPCQAPQOWEGRQVMYQ 56
Db  46  AGURPPFGSHSVWLPGLCCRCRSLCLYLLCLPSRPASWPIQGWETPLQ 98

RESULT 3
US-10-505-928-69
; Sequence 69, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 69
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-69

Query Match          6.1%; Score 74; DB 6; Length 1456;
Best Local Similarity 23.1%; Pred. No. 18;
Matches 43; Conservative 23; Mismatches 58; Indels 62; Gaps 12;

QY  1  MPCRAPLRTVPG--ALGAWLLGGLW-----AWTLGGLCSLGAVGAPRPC-----QAP 45
Db  593  MPRK-----PGCVARTGTAGGLWDVLKDEKAKFVKHWAEGVTHPPKPTTPPEKCP 647
QY  46  QWQEGRQVMYQSSGRNSRALLSY----DGLNQRVRLDERKALIPCKRLFEYILLYKDG 101
Db  648  EDW-----GASSRTSLCFKLYAKGKHEKKTWFESRDP--CRAL-----GG 685
QY  102  VMFQIQDQATKQCSKMTLTQPDWDLDPQNSTFDDQY-----SIGGPOEQITVQWSDRKA 157
Db  686  DLASINKEEQOTIWL-----ITASGSYHKLFWLGLTYGSPSEGFT---WSD-GSP 733
QY  158  RSYETW 163
Db  734  VSYENW 739

RESULT 4
US-11-318-939-13
; Sequence 13, Application US/11318939
```

```
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Soffi, Gerald
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-318-939-13

Query Match          6.0%; Score 72.5; DB 7; Length 790;
Best Local Similarity 20.1%; Pred. No. 12;
Matches 51; Conservative 22; Mismatches 98; Indels 83; Gaps 12;

QY  25  WTLGGLCSLGAVGAPRPCQAPQOWEGRQVMYQSSGRNSRALLSYDGLN---QRVRVLDE 81
Db  235  WEFCDI-----PR-CTTPPTSGTYQCLKGRGENYRGTVSVTASGHTCQRWSAQSP 285
QY  82  RK-----ALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDWDLDP---QNSTF 133
Db  286  HKHNRTPENFPCKNLEENYCRNPDG-----ETAPWCYTTDSVRWDYCKIPCGSGSTTS 339
QY  134  EDQYSIGGPOEQITVQWSDRKSARSY-----ETWIGIYTVKDCYPVQET-- 178
Db  340  TEHLDAPVPEQTPVAQDCYRGNGESYRGTSSTTITGRKQCSWVSMTPHRR-----EKTGP 395
QY  179  -----FTINYSVILSTREFFDQLGKIDPSVFTP-----PS 208
Db  396  NFPNAGLTWNY-----CRNPAD---KSPWCYTTDRVRWEYCNLKKCSETEQOVTFNFA 447
QY  209  TCQMAQLEKMSDC 222
Db  448  IAQVPSVEDLSDC 461

RESULT 5
US-10-953-349-24222
; Sequence 24222, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 24222
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24222

Query Match          5.7%; Score 69.5; DB 6; Length 413;
Best Local Similarity 21.1%; Pred. No. 11;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;
```



```

;
; CURRENT APPLICATION NUMBER: US/11/293,697
;
; CURRENT FILING DATE: 2005-12-05
;
; PRIOR APPLICATION NUMBER: US/10/108,260
;
; PRIOR FILING DATE: 2002-03-28
;
; NUMBER OF SEQ ID NOS: 5458
;
; SOFTWARE: PatentIn ver. 2.1
;
; SEQ ID NO 3610
;
; LENGTH: 802
;
; TYPE: prt
;
; ORGANISM: Homo sapiens
;
; US-11-293-697-3610

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Query Match 5.7%; Score 69; DB 7; Length 802;
Best Local Similarity 29.1%; Pred. No. 28;
Matches 30; Conservative 9; Mismatches 38; Indels

Qy	128	PQNSTFDOYS-----IGGP-OEQITVQWESDRKARSRYETWII
	:	: : : :
Db	461	PSTATFDQLTPSSATPPDPIPLPGGOUT-----ETSRSYED----
	:	: : : :
Qy	178	TFTINYSVILSTRFFDIQLGKDPSVFPTTCTCMAQLEKMS 220
	:	: : : :
Db	505	TSFPFDLLSTATFPPLGPSAHEOLTFPSTFAOHLDDPSO 547
	:	: : : :

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RESULT 13
US-10-953-349-5105
; Sequence 5105, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al
; TITLE OF INVENTION: SEQUENCE-DETERMIN
; METHOD FOR IDENTIFYING ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5105
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5105

```

Query Match	5.6%;	Score 67.5;	DB 6;	Length 294;
Best Local Similarity	19.4%;	Pred.No.11;		
Matches	38;	Conservative 26;	Mismatches 57;	Indels 73; Gaps 9;
Qy	52	QVMYQSSGRNALLSYDGI---	NORVLDERKALIPKRLFEVILLYK-----	99
Db	46	KVMGSSMTEAERLLASALEHDSNORFVLLSDR----	CAPLYDFGYIKYLISSPRS	100
Qy	100	-----	-----	-----
Db	101	FVDSFLHTKETRYSVKMSPIPBEEKWRKGSQWIALIRSHAENVINDGIVPFVFEKFKRC	160	
Qy	114	SKMTLLQPWPLDIPQNSTFDDQYSIGGPEQITVQWSDRKSAR--SYETW--IGI-YT	168	
Db	161	PLPGTNEAWFLFKQKRNCIPDEHYV---QTLTMOGLESEMERRTVITYTWNVSGTKYE	217	
Qy	169	KDCYCPVQETFTINYS	184	
Db	218	AKSWHPV--TFTLENS	231	

RESULT 14
US-10-953-349-5104
; Sequence 5104, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al
; TITLE OF INVENTION: SEQUENCE-DETERMIN
; TITLE OF INVENTION: ENCODED THERBY

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; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5104
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5104

```

Query Match	5.6%	Score 67.5;	DB 6;	Length 383;
Best Local Similarity	19.4%;	Pred.No.16;		
Matches	38;	Conservative	28;	Mismatches 57; Indels 73; Gaps 9
Qy	52	QVMYQQSSGRNSRALLSYDGL-----NQRVRLDERKALIPCKRLFEEVILLYK-----	99	
	:	:::	:	:
	:	:	:	:
	:	:	:	:
Db	135	KVVWGESSMIEAERLLLASALEDSHNRQFVLSDR-----CAPLYDFGIYKYLLISSPRS	189	
Qy	100	-----DGWMFOI--DOATKQC	113	
	:	:	:	:
	:	:	:	:
Db	190	FVDSFLTKETRYSVKMSPVIPBEKMRKGSQWIALIRSHAENVINDGIVFPVFKEFCRCR	249	
Qy	114	SKMTLTQPWPDLDPONSTFEDOVYSIGGPQEITVQWSDRKSAR--SYETW--IGI-YT	168	
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	250	PLPGTNEAWLFLQKRNCNPDEHYV---QTLLTMQGLESEMERVTYYTVNVVSGETKYE	306	
Qy	169	VKDCYPVQETFTINYS	184	
	:	:	:	:
	:	:	:	:
Db	307	AKSWHPV--TFTLENS	320	

```

RESULT 15
US-10-953-349-5103
; Sequence 5103, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al
; TITLE OF INVENTION: SEQUENCE-DETERMIN
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5103
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5103

```

Query Match	5.6%;	Score 67.5;	DB 6;	Length 439;
Best Local Similarity	19.4%;	Pred. No. 19;		
Matches	38;	Conservative 28;	Mismatches 57;	Indels 73; Gaps 9
Qy	52	QVMYQOSSGRNALLSYDGL	---NORVAVLDERKALIPCKRLFEVILLYK	----- 99
Db	191	KVMWGSSMTEARLLLSALEDHNRQFVLLSDR	-----CAPLYDFGYIKYLLISSPRS	245
Qy	100	-----	DGVMFOI--QOATKQC	113
Db	246	FVDSFHLTKETRYSVKMSVPVPEEKWRKGSQWIALIRSHAQVIVNDGIVFPVFKEFCRC	305	
Qy	114	SKMTLTQPMPLDIPONSTFEDQYSIGGPOEITVQESDRKSAR	--SYETW--IGI-YT	168
Db	306	PLPGTNEAWFLQKRRNCIPDEHYV	---QTLTMOGLESEMERRTYTYTVNVSQTKYE	362
Qy	169	KDCYCPVQETFTINYS	184	
Db	363	AKSWHPV--TFTLENS	376	

Search completed: June 10, 2006, 03:02:05

Job time : 17 secs



GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:01:59 ; Search time 199 Seconds
(without alignments)
429.646 Million cell updates/sec

Title: US-10-733-646-2_COPY_38_224

Perfect score: 1005
Sequence: 1 APRPCAPQWEGRQVMYQQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1005	100.0	224	2 AAW51119	AAW51119 Human epe
2	1005	100.0	224	2 AAY06511	AAY06511 Human epe
3	1005	100.0	224	3 AAY94654	AAY94654 Human hom
4	1005	100.0	344	9 ADY18068	ADY18068 PRO polyp
5	886	88.2	224	2 AAW51120	AAW51120 Rat epend
6	875	87.1	224	2 AAW51121	AAW51121 Mouse epe
7	875	87.1	224	3 AAY94655	AAY94655 Murine ho
8	281	28.0	210	6 ABR40123	ABR40123 Human cel
9	84.5	8.4	931	8 ADL72200	ADL72200 Mouse sal
10	84	8.4	426	4 AAB70789	AAB70789 N. magada
11	82.5	8.2	1572	5 ABP65360	ABP65360 Bifidobac
12	82	8.2	419	5 ABP39813	ABP39813 Staphyloc
13	82	8.2	419	8 ADS05801	ADS05801 Staphyloc
14	81	8.1	970	7 ADD68250	ADD68250 Murine OS
15	81	8.1	970	9 ADL26698	ADL26698 Soluble m
16	81	8.1	970	9 AED01101	AED01101 Mouse onc
17	79.5	7.9	996	9 ADX39977	ADX39977 HIV Pol p
18	79.5	7.9	2548	2 AAY05781	AAY05781 Human myo
19	79.5	7.9	2548	7 ADES5538	ADES5538 Human Pro
20	79	7.9	144	6 ABU43346	ABU43346 Protein e
21	79	7.9	611	3 AAG41475	AAG41475 Arabidops
22	78	7.8	1541	8 ADL91598	ADL91598 Yeast rap
23	77	7.7	469	7 ADG63082	ADG63082 Mouse per

ALIGNMENTS

RESULT 1

AAW51119
ID AAW51119 standard; protein; 224 AA.

XX AC AAW51119;

DT 06-NOV-1998 (first entry)

XX Human endodymin-like protein.

DE Human endodymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.

XX Homo sapiens.

XX Location/Qualifiers

FT Peptide
/note= "Signal peptide; This sequence is claimed by the inventors under claim 10 in the specification"

FT Peptide
25..137

FT /note= "This sequence represents another signal peptide which is part of the precursor protein (residues 25-224); the precursor protein claimed by the inventors under claim 9 in the specification"

FT Protein
/note= "Human endodymin-like protein; This sequence is claimed by the inventors under claim 2 in the specification"

XX WO9811130-A2.

XX 19-MAR-1998.

XX 10-SEP-1997; 97WO-JP003194.

XX 11-SEP-1996; 96JP-00240880.

XX 28-NOV-1996; 96JP-00318049.

XX 27-MAY-1997; 97JP-00135633.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Ogi K, Onda H;

XX WPI; 1998-250952/22.

CC endodymin activity. Human endodymin can be used to treat conditions in
 CC patients having need of the endodymin protein. Conditions that can be
 CC treated or detected are nervous system-related disorders, such as
 CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,
 CC pain, stroke, depression, anxiety, epilepsy and other neurological or
 CC psychiatric disorders. Diagnosis of cancers of the nervous system is also
 CC included. Endodymin, or its agonists or antagonists may also be used to
 CC treat disorders of the blood-brain barrier since endodymin participates
 CC in the endothelial cell barrier by modulating cell-matrix interactions.
 CC Antagonists may inhibit formation of endodymin-collagen fibrils, which
 CC cover endothelial cells of numerous blood vessels, hence anti-endodymin
 CC antibodies may regulate angiogenesis
 XX

SQ Sequence 224 AA;

Query Match 100.0%; Score 1005; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.1e-103;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGRWVYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 60
 DB 38 APRPCAPQWEGRWVYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 97

QY 61 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 120
 DB 98 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 157

QY 121 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPSVTPPSTCMAQLEK 180
 DB 158 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPSVTPPSTCMAQLEK 217

QY 181 MSEDCSW 187
 DB 218 MSEDCSW 224

RESULT 3

AAAY94654
 ID AAY94654 standard; protein; 224 AA.

AC AAY94654;

XX 29-AUG-2000 (first entry)

XX Human homology to endodymin-like protein (HELP) amino acid sequence.

XX Homology to endodymin-like protein; HELP; chromosome 7p14-12;
 KW central nervous system disorder; peripheral nervous system disorder;
 KW Alzheimer's disease; memory loss; stroke; neuronal damage;
 KW osteoblast differentiation; proliferation; stimulation; bone wear;
 KW arthritis; osteoporosis; cerebral cavernous malformation;
 KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..37

FT /label= Putative signal peptide

FT Protein 38..224

FT /label= Homology to endodymin-like protein

XX WO200032746-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028341.

XX 30-NOV-1998; 98US-00201442.

XX (MILL-) MILLENNIUM PHARM INC.

XX Pan Y;

XX

DR WPI; 2000-412299/35.
 XX N-PSDB; AAA27982.
 XX New nucleic acid molecules, designated NEL, useful for treating
 PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and
 PT neuronal damage (e.g. stroke).
 XX
 PS Claim 9; Fig 4; 97pp; English.

XX This sequence represents a human homology to endodymin-like protein
 CC (HELP) amino acid sequence. Endodymin is a protein that is involved in
 CC memory and neuronal regeneration. The human HELP gene is located on
 CC chromosome 7p14-12. Northern analysis of HELP expression showed that an
 CC approximately 3kB HELP transcript is expressed in the brain, heart, and
 CC skeletal muscle. HELP is a secreted protein. Modulators of HELP
 CC expression or activity can be used to treat disorders of the central
 CC nervous system or peripheral nervous system, e.g. neuronal disorders,
 CC memory associated disorders, such as Alzheimer's disease or stroke, or to
 CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of
 CC HELP expression or activity may be useful for modulation of osteoblast
 CC differentiation, stimulation or proliferation. They may also be used to
 CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders
 CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.
 CC The present invention also relates to a secreted protein with homology to
 CC netrin, called netrin like protein or NEL. NEL is also referred to as
 CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of
 CC NEL include interacting with the protein encoded by deleted in colorectal
 CC cancer, modulation of axon growth, migration and development, modulation
 CC of development of the nervous system, and modulation of the guidance of
 CC central nervous system commissural axons and peripheral motor axons
 XX

SQ Sequence 224 AA;

Query Match 100.0%; Score 1005; DB 3; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.1e-103;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGRWVYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 60
 DB 38 APRPCAPQWEGRWVYQSSGNRALLSYDGLNORVRLDERKALIPCKRLFEYILL 97

QY 61 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 120
 DB 98 YKGVMPFQIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 157

QY 121 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPSVTPPSTCMAQLEK 180
 DB 158 RSVETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPSVTPPSTCMAQLEK 217

QY 181 MSEDCSW 187
 DB 218 MSEDCSW 224

RESULT 4

ADY18068

ID ADY18068 standard; protein; 344 AA.

XX AC ADY18068;

XX 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 3874.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

PN

```
XX 24-FEB-2005.
XX PD
XX PF 11-AUG-2004; 2004WO-US026249.
XX PR 11-AUG-2003; 2003US-0493546P.
XX (GETH ) GENENTECH INC.
XX PA
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WT, Wu TD;
XX WPI; 2005-102330/19.
XX DR
XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX PS Claim 8; SEQ ID NO 3874; 150pp; English.
XX CC The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX CC composition, and method are useful for diagnosing and treating an immune
XX CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX CC arthritis. The present sequence represents a PRO polypeptide.
XX SQ Sequence 344 AA;
Query Match 100.0%; Score 1005; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.8e-103;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRCPAQWEGRQVYQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
DB 158 APRCPAQWEGRQVYQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 217
QY 61 YKGVNMFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 120
DB 218 YKGVNMFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 277
QY 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVTPPSTCQMAQLEK 180
DB 278 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVTPPSTCQMAQLEK 337
QY 181 MSEDCSW 187
DB 338 MSEDCSW 344
RESULT 5
ID AAW51120
AA AAW51120 standard; protein; 224 AA.
XX AC AAW51120;
XX 06-NOV-1998 (first entry)
XX DE Rat ependymin-like protein.
XX KW Rat ependymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.
XX OS Rattus sp.
XX FH
XX FT Key Location/Qualifiers
XX FT Peptide 1..34
XX FT /note= "signal peptide; This sequence is claimed by the
XX FT inventors under claim 10 in the specification"
XX FT Protein
XX FT 35..224
XX FT /note= "Rat ependymin-like protein; This sequence is
XX FT claimed by the inventors under claim 2 in the
XX FT specification"
```

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XX WO9811130-A2.
XX PD
XX PF 19-MAR-1998.
XX PR 10-SEP-1997; 97WO-JP003194.
XX PR 11-SEP-1996; 96JP-00240880.
XX PR 28-NOV-1996; 96JP-00318049.
XX PR 27-MAY-1997; 97JP-00135633.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Ogi K, Onda H;
XX WPI; 1998-250952/22.
XX N-PSDB; AAV07201.
XX New isolated ependymin-like protein - used to develop products for
XX treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia
XX or cerebellar degeneration.
XX Claim 2, 9, 10; Fig 2A-2C; 147pp; English.
XX The present sequence represents the rat ependymin-like protein. The
XX invention also claims for the human ependymin-like protein (AAW51119) and
XX its corresponding cDNA (AAV07200), and the mouse ependymin-like protein
XX (AAW51121) and its corresponding cDNA (AAV07202). The ependymin-like
XX proteins of the invention are claimed to have nerve-extending activity,
XX neuro-regenerative activity in the central nervous system, gliocyte
XX stimulating activity or memory forming activity. These ependymin-like
XX proteins and the corresponding DNA sequences which encode them are also
XX claimed to be useful as therapeutic or prophylactic agents for
XX Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX amyotrophic lateral sclerosis, dementia or cerebellar degeneration
XX SQ Sequence 224 AA;
Query Match 88.2%; Score 886; DB 2; Length 224;
Best Local Similarity 86.5%; Pred. No. 4.2e-90;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;
QY 2 PRPCAPQWEGRQVYQSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 61
DB 39 PQCQAPQWEGRQVLYQQSSGHNSRALSYDGLNQRVRLDERKALIPCKRLFEYILL 98
QY 62 KGVNMFQIDQATKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 121
DB 99 KGVNMFQIEQATKLCAKIPLAEFPWPLDIPQNSTFEDQYSIGGPQEQIMVQWSDRRTAR 159
QY 122 SYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVTPPSTCQMAQLEK 181
DB 159 SYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKDPSPVTPPSTCQMAQLEK 218
QY 182 SEDCS 186
DB 219 KENCS 223
RESULT 6
AAW51121
ID AAW51121 standard; protein; 224 AA.
XX AC AAW51121;
XX 06-NOV-1998 (first entry)
XX DE Mouse ependymin-like protein.
XX KW Mouse ependymin-like protein; prophylactic agent; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW dementia; cerebellar degeneration; central nervous system; gliocyte;
KW memory; neuron.
```

```
XX OS Mus sp.
XX FH Key
XX FT Peptide
XX FT 1..37 Location/Qualifiers
XX FT /note= "Signal peptide; This sequence is claimed by the
XX FT inventors under claim 10 in the specification"
XX FT 38..224
XX FT /note= "Mouse ependymin-like protein; This sequence is
XX FT claimed by the inventors under claim 2 in the
XX FT specification"
XX FT
XX PN WO9811130-A2.
XX XX
XX PD 19-MAR-1998.
XX XX
XX PF 10-SEP-1997; 97WO-JP003194.
XX XX
XX PR 11-SEP-1996; 96JP-00240880.
XX PR 28-NOV-1996; 96JP-00318049.
XX PR 27-MAY-1997; 97JP-00135633.
XX XX
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX XX
XX PI Ogi K, Onda H;
XX XX
XX DR WPI; 1998-250952/22.
XX DR N-PSDB; AAV07202.
XX XX
XX PT New isolated ependymin-like protein - used to develop products for
XX PT treating e.g. Alzheimer's, Parkinson's or Huntington's disease, dementia
XX PT or cerebellar degeneration.
XX XX
XX PS Claim 2, 9, 10; Fig 3A-3D; 147pp; English.
XX XX
XX CC The present sequence represents the mouse ependymin-like protein. The
XX CC invention also claims for the rat ependymin-like protein (AAW51120) and
XX CC its corresponding cDNA (AAV07201), and the human ependymin-like protein
XX CC (AAW51119) and its corresponding cDNA (AAV07200). The ependymin-like
XX CC proteins of the invention are claimed to have nerve-extending activity,
XX CC neuro-regenerative activity in the central nervous system, gliocyte
XX CC stimulating activity or memory forming activity. These ependymin-like
XX CC proteins and the corresponding DNA sequences which encode them are also
XX CC claimed to be useful as therapeutic or prophylactic agents for
XX CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
XX CC amyotrophic lateral sclerosis, dementia or cerebellar degeneration
XX CC
XX SQ Sequence 224 AA;
XX
XX Query Match 87.1%; Score 875; DB 2; Length 224;
XX Best Local Similarity 84.9%; Pred. No. 7.1e-89;
XX Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
XX
Qy 2 PRPCAPQWEGRQVMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61
Db :|||||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
39 POPCAPQWEGRQVLYQQSSGHNRRALVSVDGLNQVRVLDERKALIPCKRLFEYILLY 98
Qy 62 KGVWFQIDQATKQCKWLTQPDPLDIPQNSTFEDQYSIGGQEQITVQWSDRSAR 121
Db :|||||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:
99 KEGVMFQIEQATKQCAKIPLESVDPLDIPQNSTFEDQYSIGGQEQILVQWSDRRTAR 158
Qy 122 SYETWIGYTKDCYPVQETFTINYSVLSTRFRFDIQLGKDPQSVFTPPSTCQMAQLCKM 181
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
159 SYETWIGYVTAQKCPVQETFTIRNYTVVMSTRFRFDVQLGKDPQSVFTPPSTCQMAQLCKM 218
Qy 182 SEDCS 186
Db :|:|
219 SDGCS 223
XX
XX RESULT 7
XX AAY94655
XX ID AAY94655 standard; protein; 224 AA.
```

```
XX AC AAY94655;
XX DT 29-AUG-2000 (first entry)
XX DE Murine homology to ependymin-like protein (HELP) amino acid sequence.
XX KW Homology to ependymin-like protein; HELP; Alzheimer's disease; stroke;
XX KW central nervous system disorder; peripheral nervous system disorder; NEL;
XX KW neuronal damage; memory loss; osteoblast differentiation; proliferation;
XX KW stimulation; bone wear; arthritis; osteoporosis; netrin like protein;
XX KW cerebral cavernous malformation; Charcot-Marie-Tooth syndrome; mouse.
XX OS Mus sp.
XX XX
XX FH Key
XX FT Peptide
XX FT 1..37 Location/Qualifiers
XX FT /label= Putative signal peptide
XX FT 38..224
XX FT Protein
XX FT /label= Homology to ependymin-like protein
XX PN WO200032746-A2.
XX XX
XX PD 08-JUN-2000.
XX XX
XX PF 30-NOV-1999; 99WO-US028341.
XX XX
XX PR 30-NOV-1998; 98US-00201442.
XX XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX XX
XX PI Pan Y;
XX XX
XX DR WPI; 2000-412299/35.
XX DR N-PSDB; AAA27983.
XX XX
XX PT New nucleic acid molecules, designated NEL, useful for treating
XX PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and
XX PT neuronal damage (e.g. stroke).
XX XX
XX PS Claim 9; Fig 3; 97pp; English.
XX XX
XX CC This sequence represents a mouse homology to ependymin-like protein
XX CC (HELP) amino acid sequence. Ependymin is a protein that is involved in
XX CC memory and neuronal regeneration. HELP is a secreted protein. Northern
XX CC analysis of HELP expression showed that an approximately 3kb HELP
XX CC transcript is expressed in the brain, heart, and skeletal muscle. HELP is
XX CC expressed in a punctate manner throughout adult mouse brain, suggesting
XX CC that it is expressed by neurons, it is also expressed in the membrane
XX CC surrounding the placenta. Modulators of HELP expression or activity can
XX CC be used to treat disorders of the central nervous system or peripheral
XX CC nervous system, e.g. neuronal disorders, memory associated disorders,
XX CC such as Alzheimer's disease or stroke, or to treat neuronal damage. HELP
XX CC polypeptides, nucleic acids and modulators of HELP expression or activity
XX CC may be useful for modulation of osteoblast differentiation, stimulation
XX CC or proliferation. They may also be used to treat cartilage or bone
XX CC wearing, arthritis or osteoporosis, disorders such as cerebral cavernous
XX CC malformation and Charcot-Marie-Tooth disease. The present invention also
XX CC relates to a secreted protein with homology to netrin, called netrin like
XX CC protein or NEL. NEL is also referred to as TANGO 205 or T205. Netrin is a
XX CC chemottractant. Biological activities of NEL include interacting with
XX CC the protein encoded by deleted in colorectal cancer, modulation of axon
XX CC growth, migration and development, modulation of development of the
XX CC nervous system, and modulation of the guidance of central nervous system
XX CC commissural axons and peripheral motor axons
XX XX
XX SQ Sequence 224 AA;
XX
XX Query Match 87.1%; Score 875; DB 3; Length 224;
XX Best Local Similarity 84.9%; Pred. No. 7.1e-89;
XX Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
XX
Qy 2 PRPCAPQWEGRQVMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILLY 61
```

Db 39 PQPCQAPQWEGRQVLVYQSSGHNRRALVSDGLNQRVRLDERKALIPCKRLFEVILLY 98
QY 62 KCGVMFQIDQATKQCSKMTLTQPDLPDIPQNSTFEDQYSIGGPQBITVQWSDRSAR 121
Db 99 KEGVMFQIEQATKQCAKIPLVESWDPDLPQNSTFEDQYSIGGPQEQILVQWSDRRTAR 158
QY 122 SYETWIGYTVKDCYPVQETFTTNYSVILSTRFEDIQGHKDPSTVTPSTCQMAQLEKM 181
Db 159 SYETWIGVYTAQDCYPVQETFIIRNYTVWVNSTRFEDVQLGKDPSTVTPSTCQAAQPEKM 218
QY 182 SEDCS 186
Db 219 SDGCS 223
RESULT 8
ABR40123
ID ABR40123 standard; protein; 210 AA.
XX ABR40123;
XX
DT 04-JUL-2003 (first entry)
DE Human cell adhesion and extracellular matrix protein, CADECM-20.
DE
XX
KW Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
KW anticonvulsant; nootropic; neuroprotective; immunosuppressive;
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KW gene therapy; cell adhesion; extracellular matrix; CADSCM;
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
KW atherosclerosis.
XX
OS Homo sapiens.
XX
XX WO2003027230-A2.
XX
XX 03-APR-2003.
XX
XX 02-AUG-2002; 2002WO-US024649.
XX
XX 03-AUG-2001; 2001US-0309364P.
XX 03-AUG-2001; 2001US-0310119P.
XX 17-AUG-2001; 2001US-0313091P.
XX 31-AUG-2001; 2001US-0316771P.
XX 07-SEP-2001; 2001US-0317896P.
XX 21-SEP-2001; 2001US-0324781P.
XX 05-OCT-2001; 2001US-0327606P.
XX 12-OCT-2001; 2001US-0328960P.
XX 09-NOV-2001; 2001US-0344471P.
XX 17-MAY-2002; 2002US-0381291P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
PI Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
PI Kallick DA, Xu Y, Honcheil CD, Baughn MR, Gietzen KJ, Lee S;
PI Walia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX
XX WPI; 2003-354645/33.
DR N-PSDB; ACC00411.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
XX Claim 1; Page 203; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and

CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
CC sequences (ACC00392-ACC0413 and ABR40104-ABR40125). The coding sequences
CC and proteins are useful in diagnosing, treating and preventing disorders
CC associated with aberrant expression of CADECM, such as immune system
CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
CC proliferative disorders (e.g. cancer or atherosclerosis)
XX
SQ Sequence 210 AA;
Query Match 28.0%; Score 281; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.6e-22; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0;
QY 1 APRPCAPQWEGRQVWYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKR 53
Db 158 APRPCAPQWEGRQVWYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKR 210
RESULT 9
ADL72200
ID ADL72200 standard; protein; 931 AA.
XX
XX ADL72200;
XX
XX 20-MAY-2004 (first entry)
XX
XX Mouse salt-inducible kinase 2 (SIK2) enzyme.
XX
XX SIK2; salt-inducible kinase 2; cAMP; antidiabetic; anorectic;
KW hypotensive; antiarteriosclerotic; mouse; enzyme.
XX
XX Mus musculus.
XX
XX WO2004018669-A1.
XX
XX 04-MAR-2004.
XX
XX 20-AUG-2003; 2003WO-JP010535.
XX
XX 21-AUG-2002; 2002JP-00240092.
XX 31-JAN-2003; 2003JP-00023295.
XX
XX (PROT-) PROTEIN EXPRESS CO LTD.
XX (TAKE/) TAKEMORI H.
XX (OKAM/) OKAMOTO M.
XX
XX Takemori H, Okamoto M;
XX
XX WPI; 2004-238976/22.
XX N-PSDB; ADL72199.
XX
XX Salt inducible kinases 2 and antibodies against them for treatment of
PT diabetes, obesity, hypertension, arteriosclerosis, circulatory disorders.
XX
XX Claim 1; SEQ ID NO 2; 133pp; Japanese.
XX
XX The invention relates to salt-inducible kinase (SIK) 2 polypeptides and
XX encoding polynucleotides that may control the translation activity of a
XX gene under the control of a cAMP response sequence. The SIK2 polypeptides
XX and polynucleotides may be used in medical compositions for treating and
XX detecting diabetes, obesity, hypertension, arteriosclerosis, circulatory
XX disorders and high uric acid levels in the blood. The present sequence
XX represents a mouse salt-inducible kinase 2 polypeptide.
XX
SQ Sequence 931 AA;
Query Match 8.4%; Score 84.5; DB 8; Length 931;
Best Local Similarity 22.9%; Pred. No. 13;
Matches 57; Conservative 33; Mismatches 80; Indels 79; Gaps 14;

CC used for preventing and/or treating diarrhoea brought about by pathogenic
CC bacteria and/or rotavirus. The carrier is a food composition selected
CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented
CC products, ice-creams, fermented cereal based products, milk based
CC powders, infant formula, pet food or a pharmaceutical composition
CC selected from tablets, liquid bacterial suspensions, dried oral
CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
CC (i) is useful in DNA arrays or chips to carry out analysis of the
CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
CC Bifidobacterium related nucleotide sequences given in the Sequence
CC Listing from the present invention but not mentioned further within the
CC specification. N.B. The sequence data for this patent is not represented
CC in the printed specification but is based on sequence information
CC supplied by the European Patent Office

XX SQ Sequence 1572 AA;

Query Match 8.2%; Score 82.5; DB 5; Length 1572;
Best Local Similarity 22.7%; Pred. No. 47;
Matches 40; Conservative 25; Mismatches 66; Indels 45; Gaps 8;
QY 23 GRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKGV----MFQIDQATKQCSK 78
DB 980 GDAKVTWNFDGLDAK---LAEAKA-----CDNTAVAGTQLDDTTIALK 1022
QY 79 ----MTLTQPDWPLDIPQNSTFEDQ---YSIGPQEQITVQEWSDRKSARSYETWIGIYT 131
DB 1023 GTIYVTAATPENVADTASNLTVTNQQTYSKGDQMKLT-----DDTSAEAWVTW----N 1074
QY 132 VKDCYPVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAOLEKMSDCSW 187
DB 1075 AKNDYSASPTATVNGEEREVTGLTITYGDKAPA-----SAKAEYTTDGTW 1121

RESULT 12
ABP39813
ID ABP39813 standard; protein; 419 AA.
AC ABP39813;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4658.
XX

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
XX

OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-0055779P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX

XX Doucette-Stamm LA, Bush D;
PI
XX WPI; 2002-381255/41.
DR N-PSDB; ABN92358.
DR

XX Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 4658; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have

CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site

XX SQ Sequence 419 AA;

Query Match 8.2%; Score 82; DB 5; Length 419;
Best Local Similarity 26.1%; Pred. No. 7.8;
Matches 42; Conservative 19; Mismatches 60; Indels 40; Gaps 8;
QY 39 VRVLDERKALIPCKRLFEYILLYKGVMFQIDQATK-----OCSKMTLTQ-----P 84
DB 19 VESLDE-----SLYEIVSQICEVKLGQKALKNYNLQFDQVETEKLEQSQLKNA 70
QY 85 WPLDIPQNSTFEDQYS-IGGPQEQITVQEWSDRKSARSYETW-----IGIYTV--KDCY 136
DB 71 YDMLONETRDALQEQSYQRIKVKYQENIKVKQESSQQT-ECYERHPIERVGIYVPGGKASY 129
QY 137 PVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQ 177
DB 130 P-----STVLTATLAQVAGVNEITVTPPQNSGICQ 161

RESULT 13
ADS05801
ID ADS05801 standard; protein; 419 AA.
XX
AC ADS05801;
XX

DT 04-NOV-2004 (first entry)

XX Staphylococcus epidermis polypeptide seqid 5096.

XX antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
KW recombinant expression vector; infection; computer readable medium;
KW computer based system.

XX Staphylococcus epidermidis.

XX US2004147734-A1.

XX 29-JUL-2004.

XX 01-DEC-2003; 2003US-00724972.

XX 08-NOV-1997; 97US-0064964P.

XX 13-AUG-1998; 98US-00134001.

XX 29-NOV-1999; 99US-00450969.

XX (DOUC/) DOUCETTE-STAMM L.

XX (BUSH/) BUSH D.

XX Doucette-Stamm L, Bush D;

XX WPI; 2004-580138/56.

XX N-PSDB; ADS02029.

XX New isolated polypeptide and encoding nucleic acid derived from
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
PT treating an S. epidermidis bacterial infection.

XX Claim 17; SEQ ID NO 5096; 741pp; English.

XX The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
CC vector; a cell comprising a recombinant expression vector of (1);

CC producing an *S. epidermidis* polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for *S. epidermidis* infection; a recombinant or substantially
CC pure preparation of an *S. epidermidis* polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection; detecting the presence of a *Staphylococcus* nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the *Staphylococcus* genome of
CC commercial importance; a computer based system for identifying fragments
CC of the *Staphylococcus* plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the *Staphylococcus*
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the *Staphylococcus* genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an *Staphylococcus* epidermidis bacterial
CC infection. This is the amino acid sequence of a *S. epidermidis* protein of
CC the invention.
XX
SQ Sequence 419 AA;

Query Match 8.2%; Score 82; DB 8; Length 419;
Best Local Similarity 26.1%; Pred. No. 7.8;
Matches 42; Conservative 19; Mismatches 60; Indels 40; Gaps 8;
QY 39 VRVLDERKALIPCKRLFEYLLYKDGVMFOIDQATK-----QCSKMTLQ-----P 84
19 VESLDE-----SLYEIVSQICEEVKLGQDKALKNNYLFQDVTEKLEQSQKNA 70
QY 85 WDLPLDPQNSTFFEDQYS-IGGPQQTIVQWSDRKSARSYETW-----IGYTV--KDCY 136
DB 71 YDMLDNETRDALQESYQRIKYYQENIKVQESSQOT-ECYERHPIERVGIYVPGKASY 129
QY 137 PVQETFTINYSVILSTRFFDIQLGIKDPSTFTTPSTCMAQ 177
DB 130 P-----STVLMTATLAQVAGVNEITVTVPQNSGICQ 161

RESULT 14
ADD68250
ID ADD68250 standard; protein; 970 AA.
XX
AC ADD68250;
XX
DT 15-JAN-2004 (first entry)
XX
DE Murine OSMRbeta polypeptide SEQ ID NO:120.
XX
KW mouse; zcytor17; antiinflammatory; dermatological; immunosuppressive;
KW antimicrobial; vaccine; inflammatory disease; inflammatory bowel disease;
KW ulcerative colitis; Crohn's disease; atopic dermatitis; eczema;
KW psoriasis; endotoxaemia; septicemia; toxic shock syndrome;
KW infectious disease.
XX
OS Mus musculus.
XX
PN W02003060090-A2.
XX
PD 24-JUL-2003.
XX
PF 21-JAN-2003; 2003WO-US001984.
XX
PR 18-JAN-2002; 2002US-0350325P.
PR 25-APR-2002; 2002US-0375323P.
PR 19-DEC-2002; 2002US-0435315P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sprecher CA, Kuijper JL, Dasovich MM, Grant FU, Hammond AK;
PI Novak JE, Gross JA, Dillon SR;
XX

DR WPI; 2003-618179/58.
XX N-PSDB; ADD68249.
PT New zcytor17 ligand polypeptides, useful for treating inflammatory
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
PS Example 38; SEQ ID NO 120; 372pp; English.
XX
CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC polypeptide of the invention has antiinflammatory, dermatological,
CC immunosuppressive, and antimicrobial activity, and may have a use in a
CC vaccine. The polypeptide is useful for treating inflammatory diseases,
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
CC shock syndrome or infectious diseases. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 970 AA;

Query Match 8.1%; Score 81; DB 7; Length 970;
Best Local Similarity 23.7%; Pred. No. 34;
Matches 33; Conservative 24; Mismatches 60; Indels 22; Gaps 6;
QY 17 MYQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYLLYKD-----GV 65
DB 597 IFERSVEHKARLVEKQRGYQELAPLVNPKVEIPYSTPNSFVLWPDYDSDFQAGFIKGY 656
QY 66 MFQIDQNTKQCSKMTLTQPDWDLDPONSTFFEDQYSIGGPQ-EOITVQWSDRKSARSYE 124
DB 657 LVYVKSXEMQCN-----QPWERTLLPDNSVL-CKYDINGSSTKLTVE---NLQPSLSYE 707
QY 125 TWIGIYTVKDCYPVQETFT 143
DB 708 FVTPYTSAGPGP-NETFT 725

RESULT 15
ADL26698
ID ADL26698 standard; protein; 970 AA.
XX
AC ADL26698;
XX
DT 20-MAY-2004 (first entry)
XX
DE Soluble mouse OSMRbeta receptor.
XX
KW antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
KW antibacterial; immunosuppressive; cell proliferation inhibitor;
KW immune response inhibitor; inflammatory response inhibitor;
KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
KW septicemia; toxic shock syndrome; zcytor17lig; zcytor17;
KW OSMRbeta receptor; receptor; mouse.
XX
OS Mus musculus.
XX
PN US2003215838-A1.
XX
PD 20-NOV-2003.
XX
PF 21-JAN-2003; 2003US-00351157.
XX
PR 18-JAN-2002; 2002US-0350325P.
PR 14-JUN-2002; 2002US-0389108P.
PR 19-DEC-2002; 2002US-0435361P.
XX
XX (SPRE/) SPRECHER C A.
XX (GAOZ/) GAO Z.
PA

PA (KUIJ/) KUIJPER J L.
PA (DASO/) DASOVICH M M.
PA (GRAN/) GRANT F J.
PA (PRES/) PRESNELL S R.
PA (WHIT/) WHITMORE T E.
PA (HAMM/) HAMMOND A K.
PA (NOVA/) NOVAK J E.
PA (GROS/) GROSS J A.
PA (DILL/) DILLON S R.
XX

PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ;
PI Fresnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
XX
XX
XX WPI; 2003-876545/81.
DR N-PSDB; ADL26697, ADL26699.

XX Novel multimeric or heterodimeric cytokine receptors useful for treating
PT chronic inflammatory disease such as inflammatory bowel disease,
PT ulcerative colitis, acute inflammatory disease such as endotoxemia,
PT septicemia.
XX

PS Example 38; SEQ ID NO 135; 205pp; English.

XX The invention describes an isolated multimeric or heterodimeric cytokine
CC receptor (I) having at least one polypeptide having 90 percent sequence
CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
CC acid sequence, given in specification, or at least one polypeptide
CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
CC and producing an antibody to (I) and a cytokine-binding domain of a class
CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
CC binding domain of a class I cytokine receptor and a vehicle is useful
CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
CC of hematopoietic cells and hematopoietic progenitor cells; reducing
CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
CC inflammatory disease in which zcytor17lig plays a role. The disease is a
CC chronic inflammatory disease such as inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
CC psoriasis. The disease is acute inflammatory disease such as
CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
CC An immune response inhibiting composition is useful for inhibiting an
CC immune response in a mammal exposed to an antigen or pathogen. An
CC inflammatory response inhibiting composition is useful for suppressing an
CC inflammatory response in a mammal with inflammation. An antibody that
CC specifically binds to (I) is useful for detecting the presence of a
CC multimeric or heterodimeric cytokine receptor in a biological sample.
CC This is the amino acid sequence of a DNA encoding mouse OSMRbeta receptor
CC used in the creation of a soluble mouse zcytor17-mouse OSMRbeta receptor
CC fusion protein.
XX

SQ Sequence 970 AA;

Query Match 8.1%; Score 81; DB 7; Length 970;
Best Local Similarity 23.7%; Pred. No. 34;
Matches 33; Conservative 24; Mismatches 60; Indels 22; Gaps 6;

QY 17 MYQSSGRNRALLSYDGLNQRVLDERKALIPCKRLFEVILLYKD-----GV 65
Db 597 IFERSVEHKARLVEKQRYQELAPLVNPKVEIPSTPNSFVLWPDYDSDFQAGFIKGY 656

QY 66 MFQIDQATKQCKRWTLTPQWDLDPQNSTFEDQYSIGGPQ-EQITVQEWSDRKSARSYE 124
Db 657 LVVVKSEMQCN-----QPWERTLLPDNSVL-CKYDINGSETKTLTVE---NLQPESLYE 707

QY 125 TWGIYTVKDCYPVQETFT 143
Db 708 FFVTPYTSAGFGP-NETFT 725

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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:05:54 ; Search time 40 Seconds
(without alignments)
449.813 Million cell updates/sec

Title: US-10-733-646-2_COPY_38_224

Perfect score: 1005
Sequence: 1 APRCPAQQWEGRQVMYQQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	18.0	221	2 JC1251	ependymin Om-II pr
2	173.5	17.3	221	2 JC1250	ependymin Om-I pre
3	172.5	17.2	221	2 I50538	ependymin - north
4	163	16.2	215	2 I51377	ependymin precursor
5	162	16.1	212	2 I50490	ependymin - Atlant
6	152	15.1	216	2 JU0090	ependymin precursor
7	151	15.0	217	2 A43820	ependymin precursor
8	148	14.7	216	2 A32636	ependymin II precu
9	79.5	7.9	2548	2 E59435	myosin IXA [import
10	79	7.9	257	2 C97109	specialized DNA-de
11	79	7.9	257	2 I40621	probable transcrip
12	78.5	7.8	275	2 A73219	conserved hypothet
13	78	7.8	288	2 I55184	repA protein - Bsc
14	78	7.8	1085	2 E70834	probable regulator
15	78	7.8	1541	2 S46686	hypothetical prote
16	77.5	7.7	643	2 G64412	hypothetical prote
17	76	7.6	295	2 T40061	hypothetical prote
18	75.5	7.5	600	2 H81733	DNA primase TC0175
19	75.5	7.5	685	1 E64946	oligopeptidase B (
20	74.5	7.4	615	2 PH0853	methyl-directed mi
21	74.5	7.4	632	2 S64786	hypothetical prote
22	73.5	7.3	1219	2 S54570	probable membrane
23	73.5	7.3	1720	2 T07258	cell division prot
24	73	7.3	1148	2 T13347	Cnn protein - frui
25	73	7.3	1451	2 B86286	F91.15 protein -
26	73	7.3	1641	2 T10955	early nodulin bind
27	72.5	7.2	552	2 S50313	iron transport pro
28	72.5	7.2	1442	2 C92898	DNA polymerase III
29	72	7.2	341	2 F72215	oligopeptide ABC t

30 72 7.2 363 2 D83975
31 72 7.2 440 2 T32457
32 72 7.2 839 2 G96719
33 71.5 7.1 343 1 S74943
34 71.5 7.1 483 2 S36470
35 71.5 7.1 934 2 S75633
36 71.5 7.1 1362 2 A75207
37 71 7.1 189 2 A43739
38 71 7.1 410 1 ZBBP4L
39 71 7.1 4466 1 S17653
40 70.5 7.0 147 2 H69180
41 70.5 7.0 214 2 T41805
42 70.5 7.0 595 2 F71471
43 70.5 7.0 615 2 B91272
44 70.5 7.0 615 2 B86113
45 70.5 7.0 627 2 S50583

ALIGNMENTS

RESULT 1

JC1251

ependymin Om-II precursor - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1251
R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.
Gene 118, 189-196, 1992

A:Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and

A:Reference number: JC1250; MUID:92380503; PMID:1511892

A:Accession: JC1251

A:Molecule type: mRNA

A:Residues: 1-221 <MUE>

A:Cross-references: UNIPROT:P28771; UNIPARC:UPI000012A096; GB:M93698; NID:G213413; PID:

C:Comment: This protein shares several characteristics with soluble glycoproteins medi

C:Genetics:

A:Gene: Om-II

C:Superfamily: ependymin

C:Keywords: glycoprotein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-221/Product: ependymin Om-II #status predicted <MAT>

F:33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.0%; Score 180.5; DB 2; Length 221;
Best Local Similarity 25.3%; Pred. No. 4e-10;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;

Qy 2 PRCPAQQWEGRQVMYQQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY 61

Db 26 PQHCTSPNMTGVLTVMALTGGEIKATGHYSYDSTNKKLRFTESEMHNLKTEHLEDYLMFL 85

Qy 62 KGVNFQIDQATKQCKMTLTQPDWPLDIPQNSTFEDQYSIGG---PQEQITVQWSBRK 118

Db 86 EEGVFYDIDMKQCKMSLHSHAHLELPAGAAHQVELFLGSDTVQEDNKKVNTWMG-S 144

Qy 119 SARSEYEWIGYTVKDCVPVQETFTINVSVLTRFRFPDIQLGIDKPSVFTPEPSTCQMAQL 178

Db 145 VAETKGQYSALTTVGECLPL-STFYSTDSTITLLFSNSEVTVTKAPENFTLPSFCEAVEL 203

Qy 179 EK 180

Db 204 EE 205

RESULT 2

JC1250

ependymin Om-I precursor - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1250; PC1124

R:Mueller-Schmid, A.; Rinder, H.; Lottspeich, F.; Gertzen, E.M.; Hoffmann, W.

Gene 118, 189-196, 1992

A;Title: Ependymins from the cerebrospinal fluid of salmonid fish: Gene structure and md
A;Reference number: JCI250; MUID:92380503; PMID:1511892
A;Accession: JCI250
A;Molecule type: mRNA
A;Residues: 1-221 <MUE>
A;Cross-references: UNIPROT:P28770; UNIPARC:UPI000012A092; GB:M93697; NID:g213411; PIDN:
A;Accession: PCL124
A;Molecule type: protein
A;Residues: 22-44;198-221 <MU2>
A;Cross-references: UNIPARC:UPI00001788FF; UNIPARC:UPI0000178900
C;Comment: This protein shares several characteristics with soluble glycoproteins mediat
C;Genetics:
A;Gene: Om-I
C;Superfamily: ependymin
C;Keywords: Glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-221/Product: ependymin Om-I #status experimental <MAT>
F;33,73,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.3%; Score 173.5; DB 2; Length 221;
Best Local Similarity 24.3%; Pred. No. 1.9e-09;
Matches 45; Conservative 39; Mismatches 96; Indels 5; Gaps 3;

QY 2 PRCPAQWEGROVMYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLY 61
DB 26 PQHCTSPNMTGVLTVLALTGGEIKATGHYSYDSTDKIRFTESEMHNLKTEHLEDYLMLF 85

QY 62 KDGVMFQIDQATKQCSKMTLTQPDIPQNSFFEDQYSIGG---PQEQITVQWSDRK 118
DB 86 EGVFYDIDMKNQSKCKMSLHSHAHLELPAGAAHQVLEFLGSDTVQEEEDIKNINWTSV 145

QY 119 SARYETWIGIYTKVCYPQVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQMAQL 178
DB 146 PETKGQVFLST-TVGECLPL-STFYSTDSTITLFSNSQVTVTEKAPVFNLPSCFCEGVEL 203

QY 179 EKMSE 183
DB 204 EEAPE 208

RESULT 3
150538
ependymin - northern pike
C;Species: Esox lucius (northern pike)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50538
R;Mueller-Schmid, A.; Ganss, B.; Gorr, T.; Hoffmann, W.
J. Mol. Evol. 36, 578-585, 1993
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Clu
A;Reference number: I50490; MUID:91353529; PMID:8350351
A;Accession: I50538
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-221 <MUE>
A;Cross-references: UNIPROT:P32188; UNIPARC:UPI000012A09D; GB:L09066; NID:g305096; PIDN:
C;Genetics:
A;Gene: Epd
C;Superfamily: ependymin
C;Keywords: Glycoprotein
F;37,77,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 172.5; DB 2; Length 221;
Best Local Similarity 25.8%; Pred. No. 2.4e-09;
Matches 49; Conservative 34; Mismatches 94; Indels 13; Gaps 4;

QY 2 PRCPAQWEGROVMYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFEYLLY 61
DB 30 PQHCTSPNMTGVLTVLALNGGEIKATGHYHYDITDKKLRFTESDMHNLKSEHLEDYLMLF 89

QY 62 KDGVMFQIDQATKQCSKMTLTQPDIPQNSFFEDQYSIGG---PQEQITVQEW---- 114
DB 90 EGVFYDIDLKNQSKCKMSLQSHAHLELPAGAAHQVLEFLGSDTVQEEENIKVINWTSV 149

QY 115 SDEKSARSYETWIGIYTKVCYPQVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTCQ 174
DB 150 PETKGQYSVST-----TVGDCLPL-STFYSTDSTITLFSNSQVTVTEKAPVFNLPSCFCE 203

QY 175 MAQLEKMSD 184
DB 204 GLELEDTHND 213

RESULT 4
151377
ependymin precursor - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51377
R;Adams, D.S.; Shashoua, V.E.
Gene 141, 237-241, 1994
A;Title: Cloning and sequencing the genes encoding goldfish and carp ependymin.
A;Reference number: I51377; MUID:94215910; PMID:8163195
A;Accession: I51377
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-215 <ADA>
A;Cross-references: UNIPROT:P38528; UNIPARC:UPI000012A09B; EMBL:U00432; NID:g397655; P;
C;Genetics:
A;Gene: epn
A;Introns: 28/1; 39/3; 84/3; 147/1; 175/2
C;Superfamily: ependymin

Query Match 16.2%; Score 163; DB 2; Length 215;
Best Local Similarity 24.2%; Pred. No. 2e-08;
Matches 47; Conservative 45; Mismatches 84; Indels 18; Gaps 7;

QY 3 RCPAQWEGROVMYQQSSGRNSRAL--LSYDGLNQVRVLDERKALIPCKRLFEYLL 60
DB 25 QPCHSPPLTSG--TMKVSTGTHDLASGEFSYDSKANKRFVEDTAHANKTSHM-DVLVH 81

QY 61 YKGVNMFQIDQATKQCSKMTLTQPDIPQNSFFEDQYSIGP---QEQITVQWSDR 117
DB 82 FEEGVLYEIDSKNESCKETLQFRKHLMEIPPDATHESEIYMGSPSITEQGLRVRVNWK 141

QY 118 ----KSARSYETWIGIYTKVCYPQVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTC 173
DB 142 LPELHAHYSLSLT-----TSCGCLPVSGSYGDKKDLIFS-FFGVETEVDQPVFPVPAVC 195

QY 174 QMAQLEKMSDSCSW 187
DB 196 EAVAFEEAPDDHSF 209

RESULT 5
150490
ependymin - Atlantic herring
C;Species: Clupea harengus, Clupea harengus harengus (Atlantic herring)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50490
R;Mueller-Schmid, A.; Ganss, B.; Gorr, T.; Hoffmann, W.
J. Mol. Evol. 36, 578-585, 1993
A;Title: Molecular analysis of ependymins from the cerebrospinal fluid of the orders Cl
A;Reference number: I50490; MUID:93353529; PMID:8350351
A;Accession: I50490
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-212 <MU2>
A;Cross-references: UNIPROT:P32187; UNIPARC:UPI000012A09A; GB:L09065; NID:g304576; PIDN:
C;Genetics:
A;Gene: Epd
C;Superfamily: ependymin
C;Keywords: Glycoprotein
F;69,92,112/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.1%; Score 162; DB 2; Length 212;
Best Local Similarity 23.7%; Pred. No. 2.5e-08;

Query Match 14.7%; Score 148; DB 2; Length 216;
Best Local Similarity 23.7%; Pred. No. 5.9e-07;
Matches 45; Conservative 43; Mismatches 92; Indels 10; Gaps 6;
QY 3 RPOCAPOQWEGRWVYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYILL 60
DB 26 QPCHSPPLISG--TMKWVSTGGHDLASGFSYDKANKRFRFVDAHAANKTSHT--DVLVH 82
QY 61 YKGVNMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQVSIIGP--OEOITVQWSDR 117
DB 83 FEGTUYEIDSKNESCKETLQFRKILMEIPDPATHESEIYMGSPSITEGGLRVVWSGK 142
QY 118 KSARSYETWIGIYTVKDCVPVQBTFTINYSVILSTRFFDIQLGKDPSPVFTPPSTCOMAQ 177
DB 143 LPELHAHYSLSI--TSCGCLPVSGSYGDKDLLFS--FFGVETEVDLDQVFPVPAECGVA 200
QY 178 LEKMSDECSW 187
DB 201 FEEAPDDHSF 210
RESULT 9
E59435
myosin IXA [imported] - human
C;Species: Homo sapiens (man)
C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
R;Accession: E59435
R;Gorman, S.W.; Haider, N.B.; Grieshammer, U.; Swiderski, R.E.; Kim, E.; Welch, J.W.; Se
Genomics 59, 150-160, 1999
A;Title: The cloning and developmental expression of unconventional myosin IXA (MYO9A) a
A;Reference number: E59435
A;Accession: E59435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2548 <GOR>
A;Cross-references: UNIPROT:Q9UNJ2; UNIPARC:UPI000007206F; GB:NP_008832; PID:G5902012; P
Query Match 7.9%; Score 79.5; DB 2; Length 2548;
Best Local Similarity 20.2%; Pred. No. 59;
Matches 39; Conservative 26; Mismatches 77; Indels 51; Gaps 7;
QY 4 PCQAPQWEGRWVYQSSGRNSRALI-----SYDGLNQRVRLDERKALIPCKRL 54
DB 82 PVQOMLWP--RMALENRLSGEDYRFLLRKLNKDGSIHYGSLQSLRWLRVTEERRMM--ERG 138
QY 55 FEYILLYKGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQVSIIGPQSIITVQEW 114
DB 139 F-----LPQPQQKDFDCLSLPDLNKTLLNL 166
QY 115 SDRKSARSYETWIGI-YTVKDCVPVQBTFTINYSVILSTRFFD-IQLGKDPSPVFTPPST 172
DB 167 RDRFKHEKIYTVGSILIVNPFKFLIYNPKY-----VKMYDNHQLGKPEPHIYADV 221
QY 173 COMAQLEKMSDC 185
DB 222 AYHAMLQKKNQ 234
RESULT 10
C97109
specialized DNA-dependent RNA polymerase sigma chain [imported] - Clostridium acetobutyli
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
R;Accession: C97109
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <KUR>

A;Cross-references: UNIPROT:P33658; UNIPARC:UPI0000134848; GB:AE001437; PIDN:AAK79662.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1696
C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF
Query Match 7.9%; Score 79; DB 2; Length 257;
Best Local Similarity 22.5%; Pred. No. 4;
Matches 39; Conservative 38; Mismatches 66; Indels 30; Gaps 8;
QY 12 EGRVWYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQI 69
DB 101 EIRRYLRDNNIRVSRSLRDIAVRLQVDRLLSKNNKEPTVSIKELKIPREVIKIPAL 160
QY 70 DOATKQCSKMTLTQPDPLDIPQNSTFEDQVSIIGPQSIITVQWSDRKSARSYETWIGI 129
DB 161 DAIQ-----DPI-----SLFEPIYHDDGDAIYV--MDQISDNKLD--DSWLQN 200
QY 130 YTVKDCVPVQBTFTINYSVILSTRFFD--IQLGKDPSPVFTPPSTCOMAQLEK 180
DB 201 ISIKE---AMKKLSREKMLNMRFPDGRQTQMEVADEIGI---SQAQVSRLEK 247
RESULT 11
I40621
probable transcription initiation factor sigma G - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
R;Accession: I40621; I40628; S34310
R;Sauer, U.; Treuner, A.; Buchholz, M.; Santangelo, J.D.; Durre, P.
J. Bacteriol. 176, 6572-6582, 1994
A;Title: Sporulation and primary sigma factor homologous genes in Clostridium acetobuty
A;Reference number: I40609; MUID:95050216; PMID:7961408
A;Accession: I40621
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-257 <RES>
A;Cross-references: UNIPROT:P33658; UNIPARC:UPI0000134848; EMBL:Z23079; NID:G2437821; P
R;Wong, J.; Sasse, C.; Bennett, G.N.
Gene 153, 89-92, 1995
A;Title: Sequence and arrangement of genes encoding sigma factors in Clostridium acetob
A;Reference number: I40626; MUID:95189110; PMID:7883192
A;Accession: I40628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-257 <RE2>
A;Cross-references: UNIPARC:UPI0000134848; EMBL:U07420; NID:G705344; PIDN:AAC43310.1; P
R;Sauer, U.; Treuner, A.; Buchholz, M.; Duerre, P.
submitted to the EMBL Data Library, June 1993
A;Description: Sigma factor homologous genes in C. acetobutylicum.
A;Reference number: S34306
A;Accession: S34310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 24-145, 'G', 147, 'G', 150, 'NTSPRSD', 158-257 <SAU>
A;Cross-references: UNIPARC:UPI000017576F; EMBL:Z23079
C;Genetics:
A;Gene: sigG
A;Start codon: GTG
C;Superfamily: transcription sigma factor G; transcription initiation factor sigma katF
C;Keywords: DNA binding; sigma factor; transcription initiation
F;44-257/Domain: transcription initiation factor sigma katF homology <KTF>
Query Match 7.9%; Score 79; DB 2; Length 257;
Best Local Similarity 22.5%; Pred. No. 4;
Matches 39; Conservative 38; Mismatches 66; Indels 30; Gaps 8;
QY 12 EGRVWYQSSGRNSRAL--LSYDGLNQRVRLDERKALIPCKRLFEYILLYKGVNMFQI 69
DB 101 EIRRYLRDNNIRVSRSLRDIAVRLQVDRLLSKNNKEPTVSIKELKIPREVIKIPAL 160
QY 70 DOATKQCSKMTLTQPDPLDIPQNSTFEDQVSIIGPQSIITVQWSDRKSARSYETWIGI 129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <KUR>


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Db      161  DAIQ-----DPI-----SLFPIYHDDGDAIYV-MDQISDNKNULD--DSWLQN 200
Qy      130  YTKDCYQVQFTTINYSVILSTRFD--IQLGKDPSEVTPPSTCMAOLEK 180
Db      201  ISIKE---AMKKLSPREKHLNMRFFDGRTOEVADEIGI---SOAGVSLEK 247

```

RESULT 12
A72319
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: A72319
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MID:99287316; PMID:10360571
A:Accession: A72319
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <ARN>
A:Cross-references: UNIPROT:Q9X008; UNIPARC:UPI000000C135F; GB:AE001755; GB:AE0000512; NID
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0906
C:Superfamily: Bacillus subtilis flagellar probable biosynthesis switch protein vlxH

Query Match	7.8%;	Score	78.5;	DB	2;	Length	275;
Best Local Similarity	25.2%;	Pred. No.	4.9;				
Matches	37;	Conservative	26;	Mismatches	65;	Indels	19;
						Gaps	7;

QY	21	SSGNSRALLSYDGLNQVRVLDERKALIPCKELFEYILL-YKDGWFWFOIDQATQCSKM	79
		: : : : : : : : : : : : : : : : : : : :	
Db	94	SSGIDMEDILFN-LGDRRRFFDEFARLL---RKDYILVIDPPGYNENLDQFYIQSDFL	149
		: : : : : : : : : : : : : : : : : : : :	
QY	80	TLTPQMDPLDIPONSTFEDQYSIGG--PQEQITVQEW-----SDRKSARSYETWI	127
		: : : : : : : : : : : : : : : : : : : :	
Db	150	ILVTSPTSIIINTYTLKLLSVKGIPTPEEILFVNMVVRNMKEGRLLAARDLK-RVVERFV	208
		: : : : : : : : : : : : : : : : : : : :	
QY	128	GLYTVKDCYVPVQETFTTINYSVILSTRF	154
		: : : : : : : : : : : : : : : : : : : :	
b	209	G-FTIKNYFVFIKEDQVQRSVFLQEPF	234
		: : : : : : : : : : : : : : : : : : : :	

RESULT 13

I55184

repA protein - Escherichia coli

C:Species: Escherichia coli

C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C:Accession: I55184; S34178

R:LLanes, C.; Gabant, P.; Couturier, M.; Michel-Briand, Y.

J. Bacteriol. 76, 3403-3407, 1993

A:Title: Cloning and Characterization of the Inc A/C plasmid RAI replicon.

A:Reference number: I55184

A:Accession: I55184

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: UNIPROT:Q08986; UNIPARC:UPI0000089B5C; EMBL:X73674; NID:g313284; PID

C:Genetics:

A:Gene: repA

Query Match	7.8%;	Score 78;	DB 2;	Length 288;
Best Local Similarity	24.0%;	Pred. NO. 5.8;		
Matches	37;	Conservative	34;	Mismatches 49; Indels 34; Gaps 8;
Qy	25	NSRALLSYDGLNQRVRLDE--RKALIPCKRLFEVILLYKDGVMFQIDQATQCKSM----	79	
Db	102	DGRTVLIYAG--QREILEDALRLKLVANGK--GHIIEGKAGVMFTLYELQELSKMGHG	156	
Qy	80	-TLTPDWPDLDPQNSTFDQYSIGSQPQITVQSWSDRSKARSYETWIGITVTKD----	134	

Db 157 YNLTEIKAEIQVCRGATLE-----CISDDGEAFISSSPFPMVGLTTRGEFRKK 204
 Qy 135 -----CYPVQETFTINYSVI-LSTRFFDIQLGIK 162
 Db 205 GGNARCY-VQPNPLVNESIMNLSPROYNYKIGMO 237

RESULT 14
E70834
probable regulatoryprotein with some - Mycobacterium tuberculosis (strain H37Rv)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: E70834
R/Col: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the comple
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: E70834
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1085 <COL>
A/Cross-references: UNIPROT:O53720; UNIPARC:UPI000016521A; GB:AL021931; GB:AL1
A/Experimental source: strain H37Rv
C/Genetics:
A/Gene: Rv0386

Query Match	7.8%;	Score 78;	DB 2;	Length 1085;
Best Local Similarity	22.9%;	Pred. No. 29;		
Matches	50;	Conservative	34;	Mismatches 68; Indels 66; Gaps 12
QY	5	COAPQOEWGRQVMVQ--OSSGRNSRALSXYDGLNORV----	RVLDERKALIP--CKRLFEY	57
Db	324	CREPLRVEG-EVSVRVPSLSLSDAEVEMFCYRQVRPDRFLTDDNSAAVTEICKEL---	379	
QY	58	ILLYKGVWFQIDQATKQCSKMTLTQWDPDLIDIPQNSTFEDQOYS--GGPQSIITVQ----	112	
Db	380	-----DGLPLAIELAARLSRMTLDEIIDGL-----	RDRFALLTGARTAAHRQOTL	426
QY	113	-----EWS-----DRKSASSETWIGIYTKDCVPV-----	-QSTFINYSV	148
Db	427	WASVDHSYTLITTEPRTLRLRAVFGCFPVDDAQAVACSGDVQRYQVLDEITLLVDKSL	486	
QY	149	ILSTRFFDIQLGKIDPSVFTTPPSTCQMAQ----	LEKMG	183
Db	487	VMA-----DDNSGRTCYRLCETMRHYALEKLS	514	

RESULT 15
S46686
hypothetical protein YHR186c - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein H9998.14
C:Species: *Saccharomyces cerevisiae*
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: S46686
R:Macri, C.
submitted to the EMBL Data Library, February 1994
A:Description: The sequence of *S. cerevisiae* cosmid 9998.
A:Reference number: S46674
A:Accession: S46686
A:Molecule type: DNA
A:Residues: 1-1541 <MAC>
A:Cross-references: UNIPROT:P38873; UNIPARC:UP1000013B2F6; EMBL:U00030; NID:G4444
C:Genetics:
A:Cross-references: SGD:S0001229
A:Map position: 8R
C:Keywords: transmembrane protein

Query Match	7.8%	Score 78	DB 2	Length 1541
Best Local Similarity	20.7%	Pred. No. 45		

	Matches	41;	Conservative	27;	Mismatches	74;	Indels	56;	Gaps	10;
Qy	4	PCQAPQOWEG	QVWYQSS-----	GRNSRALLSYDGLNORVRLDERKALIPCKRLFEY	57					
Db	89	PCARVEAWVD	-PLNFQDSKKAIEQIGNLQA--	OYETLSLRTRY---KQSLDFC-----	136					
Qy	58	ILLYKDGVMFQIDQATKQCSKMTLTQFWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDR	117							
Db	137	-----VEDVKRFCSNLSRRTSKEDRILFHYNH-----	GVPKPTKSGEIWFEN	178						
Qy	118	KSARSY-----	ETWIG--IYTVKDCYPVQETFTTINYSVILSTRFFDIQLGIKDPVSF	167						
Db	179	RGYTQIPVSLYDLQTLGAPCIFYVDCNSA-ENILINFQKFQKRIKDDDEGNHDAAP	237							
Qy	168	TPSTCQMAQLKMSDC	185							
Db	238	SPTSAYQ-----	DC	246						

Search completed: June 10, 2006, 03:11:20
Job time : 43 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:02:19 ; Search time 296 seconds
(without alignment)
584.385 Million cell updates/sec

Title: US-10-733-646-2_COPY_38_224

Perfect score: 1005

Sequence: 1 APRFCAPQWEGRQVYQQ.....TPPSTCQMAQLKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	100.0	224	1	EPDR1_HUMAN
2	997	99.2	344	2	Q96J80_homo sapien
3	991	98.5	224	2	Q99M77_mus musculus
4	978	97.3	227	2	Q95K54_MACFA
5	974	96.9	227	1	EPDR1_MACFA
6	941	93.6	218	2	Q95K77_MACFA
7	941	93.6	218	2	Q95K56_MACFA
8	886	88.2	224	2	Q5X110_RAT
9	875	87.1	224	2	Q99M71_m mammalian
10	869	86.5	224	2	Q8CA12_mus musculus
11	861	85.7	224	2	Q8BQV1_mus musculus
12	671	66.8	206	2	Q6DH25_BRARE
13	434.5	43.2	234	2	Q6EEF4_9ECHN
14	288	28.7	194	2	Q61WN5_BRABE
15	186	18.5	211	2	Q4TFW4_TETNG
16	181	18.0	181	2	Q90394_9TELE
17	180.5	18.0	221	1	EPD2_ONCMY
18	177.5	17.7	221	1	EPD2_SALSA
19	177	17.6	178	2	Q91083_9TELE
20	174.5	17.4	175	2	Q91140_9TELE
21	173.5	17.3	221	1	EPD1_ONCMY
22	173	17.2	178	2	Q91253_9TELE
23	173	17.2	181	2	Q91109_9TELE
24	172.5	17.2	221	1	EPD_ESOLU
25	172	17.1	178	2	Q91052_9TELE
26	164.5	16.4	183	2	Q90492_9TELE
27	163	16.2	215	1	EPD_CVBCA
28	162	16.1	212	1	EPD_CLUNA
29	158	15.7	218	1	EPD_DANAE
30	155.5	15.5	216	2	Q4S8U8_TETNG
31	154	15.3	180	2	Q91331_9TELE

32	153.5	15.3	214	1	EPD_NOTCH	Q91130_notropis ch
33	152.5	15.2	186	2	Q91465_9TELE	Q91465_synodontis
34	152	15.1	215	1	EPD1_CARAU	P13506_carassius a
35	151	15.0	217	1	EPD_BRARE	P17561_brachydanio
36	148	14.7	170	2	Q90241_9TELE	Q90241_aletes sp.
37	148	14.7	215	1	EPD2_CARAU	P12958_carassius a
38	147.5	14.7	136	2	Q91254_9TELE	Q91254_paracheirod
39	146	14.5	172	2	Q91057_9TELE	Q91057_hemiodus sp
40	132.5	13.2	140	2	Q91045_9TELE	Q91045_gasteropele
41	131	13.0	203	2	Q6WNG6_BRABE	Q6WNG6_branchiosco
42	129.5	12.9	131	2	Q90276_9TELE	Q90276_boulengerel
43	125.5	12.5	137	2	Q91058_9TELE	Q91058_hoplias sp.
44	125	12.4	192	2	Q91464_9TELE	Q91464_schilbe sp.
45	123	12.2	133	2	Q91059_9TELE	Q91059_hypostomus

ALIGNMENTS

RESULT 1

EPDR1_HUMAN STANDARD; PRT; 224 AA.
AC Q9UM22;
21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2001, sequence version 2.
DT 07-FEB-2006, entry version 40.
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).
DE protein).
GN Name=EPDR1; Synonyms=MERP1, UCC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
"Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues."
RL DNA Cell Biol. 20:625-635(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN [3]
RP NUCLEOTIDE SEQUENCE OF 51-224.
RA Nimrich I., Erdmann S., Melchers U.;
RT "Genes that are differentially expressed in colon cancer."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted protein.

```
CC -1- SIMILARITY: Belongs to the ependymin family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF361252; AAK26441.1; -; Genomic DNA.
DR EMBL; BC000686; AAK00686.2; ALT INIT; mRNA.
DR EMBL; BC018299; AAH18299.1; -; mRNA.
DR EMBL; AJ250475; CAB60269.1; ALT INIT; mRNA.
DR Ensembl; ENSG00000086289; Homo sapiens.
DR HGNC; HGNC:17572; EPDR1.
DR LinkHub; Q9UM22; -.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; 1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 37 Potential.
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT /FTID=PRO_0000008351.
FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CONFLICT 207 207 P -> S (in Ref. 3).
SQ SEQUENCE 224 AA; 25437 MW; 84ADBA3666261611 CRC64;

Query Match 100.0%; Score 1005; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. NO. 1.6e-91;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 60
DB 38 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 97
QY 61 YKGVNFIQIDQATKQCKMTLTQWPDLIPQNSTFEDQYSIGPQEQITVQWSDRKA 120
DB 98 YKGVNFIQIDQATKQCKMTLTQWPDLIPQNSTFEDQYSIGPQEQITVQWSDRKA 157
QY 121 RSYETWIGIYTKDCVPQVQETFTINYSVILSTRFFDIQLGKDPSPVFTPTSTCMAQLEK 180
DB 158 RSYETWIGIYTKDCVPQVQETFTINYSVILSTRFFDIQLGKDPSPVFTPTSTCMAQLEK 217
QY 181 MSRDCSW 187
DB 218 MSRDCSW 224

RESULT 2
Q96J80 HUMAN PRELIMINARY; PRT; 344 AA.
AC Q96J80;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Mammalian ependymin related protein 1.
GN Name=EPDR1; Synonyms=MERP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/10454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues."
RL DNA Cell Biol. 20:625-635(2001).
CC
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21940632; PubMed=11943480; DOI=10.1016/S0378-1119(02)00434-1;
RA Gregorio-King C.C., McLeod J.L., Collier F.M., Collier G.R.,
RA Bolton K.A., Van Der Meer G.J., Apostolopoulos J., Kirkland M.A.;
RT "MERP1: a mammalian ependymin-related protein gene differentially
RT expressed in hematopoietic cells."
RL Gene 286:249-257(2002).
CC -----
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CC -----
DR EMBL; AY027862; AAK15788.2; -; mRNA.
DR Ensembl; ENSG00000086289; Homo sapiens.
DR HGNC; HGNC:17572; EPDR1.
DR LinkHub; Q96J80; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN 1.
SQ SEQUENCE 344 AA; 38141 MW; 34D75B84822692DA CRC64;

Query Match 99.2%; Score 997; DB 2; Length 344;
Best Local Similarity 99.5%; Pred. NO. 1.7e-90;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 60
DB 158 APRCPAQWEGRWYQSSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILL 217
QY 61 YKGVNFIQIDQATKQCKMTLTQWPDLIPQNSTFEDQYSIGPQEQITVQWSDRKA 120
DB 218 YKGVNFIQIDQATKQCKMTLTQWPDLIPQNSTFEDQYSIGPQEQITVQWSDRKA 277
QY 121 RSYETWIGIYTKDCVPQVQETFTINYSVILSTRFFDIQLGKDPSPVFTPTSTCMAQLEK 180
DB 278 RSYETWIGIYTKDCVPQVQETFTINYSVILSTRFFDIQLGKDPSPVFTPTSTCMAQLEK 337
QY 181 MSRDCSW 187
DB 338 MSRDCSW 344

RESULT 3
Q99M77 MOUSE PRELIMINARY; PRT; 224 AA.
AC Q99M77;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Mammalian ependymin related protein 1.
GN Name=Ucc1; Synonyms=Epdr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/10454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues."
RL DNA Cell Biol. 20:625-635(2001).
CC
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CC -----
DR EMBL; AY027861; AAK15787.1; -; mRNA.
DR MGI; MGI:2152290; Epdrl.
DR MGI; MGI:2152290; Ucc1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
SQ SEQUENCE 224 AA; 25437 MW; DB6CA5A9A7289E95 CRC64;

Query Match 98.6%; Score 991; DB 2; Length 224;
Best Local Similarity 99.5%; Pred. No. 3.9e-90;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APRPCQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
DB 38 APRPCQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
QY 61 YKGVMFQIDQATKQCSKMTLTQRPDLIPQNSTFFEDQYSIGGPQEQITVQWSDRKS 120
DB 98 YKGVMFQIDQATKQCSKMTLTQRPDLIPQNSTFFEDQYSIGGPQEQITVQWSDRKS 157
QY 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTVTPSTCMAOLEK 180
DB 158 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTVTPSTCMAOLEK 217
QY 181 MSEDCSW 187
DB 218 MSEDCSW 224

RESULT 4
Q95K54 MACFA
ID Q95K54_MACFA PRELIMINARY; PRT; 227 AA.
AC Q95K54;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB066537; BAB62213.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.
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SQ SEQUENCE 227 AA; 25850 MW; 3963EAB6D5F016F4 CRC64;

Query Match 97.3%; Score 978; DB 2; Length 227;
Best Local Similarity 96.8%; Pred. No. 7.8e-89;
Matches 181; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 APRPCQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
DB 41 APRPCQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 100
QY 61 YKGVMFQIDQATKQCSKMTLTQRPDLIPQNSTFFEDQYSIGGPQEQITVQWSDRKS 120
DB 101 YKGVMFQIEQATKQCSKMTLTQRPDLIPQNSTFFEDQYSIGGPQEQIMVQWSDRKS 160
QY 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTVTPSTCMAOLEK 180
DB 161 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFDFIQLGKDPSTVTPSTCMAOLEK 220
QY 181 MSEDCSW 187
DB 221 MSEDCSW 227

RESULT 5
EPDRL MACFA
ID EPDRL_MACFA STANDARD; PRT; 224 AA.
AC Q9NOC7;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2001, sequence version 2.
DT 07-FEB-2006, entry version 31.
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1
DE protein).
GN Name=EPDRL; Synonyms=MERP1, UCC1; ORFNames=QcCE-12983;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheciae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Secreted protein.
CC -|- SIMILARITY: Belongs to the ependymin family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB046003; BAB01595.1; ALT_INIT; mRNA.
DR LinkHub; Q9NOC7; -.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; 1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 37 Potential.
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT /FTID=PRO_0000008352.
FT CARBOHYD 130 130 N-linked (GlcNAc...) (potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 224 AA; 25484 MW; 3594311D15AB4BB7 CRC64;

Query Match 96.9%; Score 974; DB 1; Length 224;
Best Local Similarity 96.8%; Pred. No. 1.9e-88;
Matches 181; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APRPCQAPQWEGRVQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
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Db 38 APRPCAPQWEGQVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL 97
QY 61 YKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSA 120
Db 98 YKDGVMFQIEQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQIMVQWSDRKS 157
QY 121 RSYETWIGIYTKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEK 180
Db 158 RSYETWIGIYTKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEK 217
QY 181 MSDCSW 187
Db 218 MSDCSW 224

RESULT 6
Q95K77 MACFA PRELIMINARY; PRT; 227 AA.
AC Q95K77;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Temporal lobe right;
RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Medulla oblongata;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M.,
RA Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
chromosomes";
RL Gene 275:31-37(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Medulla oblongata;
RA Hashimoto K., Oeada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AB063094; BAB60800.1; -; mRNA.
CC EMBL; AB097520; BAC41745.1; -; mRNA.
CC GO; GO:0005576; C:extracellular region; IEA.
CC GO; GO:0005509; F:calcium ion binding; IEA.
CC GO; GO:0007160; P:cell-matrix adhesion; IEA.
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC PRODOM; PD006315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
CC PROSITE; PS00899; EPENDYMIN_2; 1.
CC Hypothetical protein.
KW SEQUENCE 227 AA; 25821 MW; B56A77C59867DA50A CRC64;
Query Match 96.9%; Score 974; DB 2; Length 227;
Best Local Similarity 96.8%; Pred. No. 2e-88; Indels 0; Gaps 0;
Matches 181; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APRPCAPQWEGQVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL 60
Db 41 APRPCAPQWEGQVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILL 100
QY 61 YKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSA 120
Db 101 YKDGVMFQIEQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQIMVQWSDRKS 160
QY 121 RSYETWIGIYTKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEK 180
Db 161 RSYETWIGIYTKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEK 220
QY 181 MSDCSW 187
Db 221 MSDCSW 227

RESULT 7
Q95K56 MACFA PRELIMINARY; PRT; 218 AA.
AC Q95K56;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Medulla oblongata;
RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AB065535; BAB62211.1; -; mRNA.
CC GO; GO:0005576; C:extracellular region; IEA.
CC GO; GO:0005509; F:calcium ion binding; IEA.
CC GO; GO:0007160; P:cell-matrix adhesion; IEA.
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC PRODOM; PD006315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
CC PROSITE; PS00899; EPENDYMIN_2; 1.
CC Hypothetical protein.
KW SEQUENCE 218 AA; 24970 MW; 8B8524C0D986677C CRC64;
Query Match 93.6%; Score 941; DB 2; Length 218;
Best Local Similarity 96.7%; Pred. No. 3.6e-85;
Matches 175; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 APOQWEGQVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKQGV 66
Db 38 APOQWEGQVMYQSSGRNRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKQGV 97
QY 67 FQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQITVOEWSDRKSARSYETW 126
Db 98 FQIEQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPOEQIMVQWSDRKSARSYETW 157
QY 127 IGYTVKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEKSDCS 186
Db 158 IGYTVKDCYVQVQETFTTNYSVILSTRFRFDIQLGKIDPVSFTTPTSCQMAQLEKSDCS 217
QY 187 W 187

RT "high-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shinkawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impombato A., Avelar R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crowe M.B., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Humnick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Rabiei S., Mulder N., Nakano N., Nakachi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
Petrowsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
Shibata H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.H., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
Tagami T., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT (Genome Network Core Team) and the PANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=22354683; PubMed=10426685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
Maglott D.R., Makino L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrowsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirokawa T., Kondo H., Nakamura M., Sakazume N., Sato K.,
Shirokane-Kishikawa T., Konno H., Aizawa K., Arakawa T., Fukuda S.,
Hirataki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=diencephalon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Query Match 87.1%; Score 875; DB 2; Length 224;
Best Local Similarity 84.9%; Pred No. 14e-78;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
QY 2 PRPCAPQWEGRGVYQQSGNRALLSYDGLNQVRVLDKALIPCKRLFEYILLY 61
DB 39 PQCPAPQWEGRGVLYQQSGHNRALVSYDGLNQVRVLDKALIPCKRLFEYILLY 98

(Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawagawa Y., Kedzierski R.M., King P.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yagunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Niehine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ogawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad T., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawagawa Y., Kedzierski R.M., King P.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yagunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
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RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Query Match 85.7%; Score 861; DB 2; Length 224;
Best Local Similarity 84.3%; Pred. No. 3.5e-77;
Matches 156; Conservative 17; Mismatches 12; Indels 0; Gaps 0;
Qy 2 PRCPAQPOQWEGROVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY 61
Db 39 PQCPAQPOQWEGROVLVYQSSGHNRLVSYDGLNQRVRLDERKALIPCKRLFEYILLY 98
Qy 62 KQGVMFQIDQATKQCKWTLTPQWPLDIPQNSTFEDQYISGGPQEQITVOEWSDRKSAR 121
Db 99 KEGVMFQEQATKQCAKIPVSSDPLDIPQNSTFEDQYISGGPQEQITVOEWSDRRTAR 158
Qy 122 SYETWIGIYVTKQCPVQETFTTNSVILSRFRFDIQLGKIDPSVFTPPSTCQMAQLEKM 181
Db 159 SYETWIGVYTKQCPVQETFTTNSVILSRFRFDIQLGKIDPSVFTPPSTCQMAQLEKM 218
Qy 182 SEDCS 186
Db 219 SDGCS 223
RESULT 12
ID Q6DH25_BRARE PRELIMINARY; PRT; 206 AA.
AC Q6DH25;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 13.
GN Name=epdrl;
OS Brachydanio rerio (zebrafish) (Danio rerio).

Q6EEF4:
16-AUG-2004, integrated into UniProtKB/TrEMBL.
16-AUG-2004, sequence version 1.
07-FEB-2006, entry version 8.
Ependymin-related protein precursor.
Name=Epen;
Holothuria glaberrima.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Aspidochiroacea; Aspidochirotida; Holothuriidae;
OC Holothuria.
NCBI_TaxID=31192;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed:15256263; DOI=10.1016/j.gene.2004.03.023;
RA Suarez-Castillo E.C., Medina-Ortiz W.E., Roig-Lopez J.L.,
RA Garcia-Ararras J.E.;
RA "Ependymin, a gene involved in regeneration and neuroplasticity in
RT vertebrates, is overexpressed during regeneration in the echinoderm
RT Holothuria glaberrima.";
RL Gene 334:133-143(2004).

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CC EMBL; AY383544; AAR89380.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR ProDom; PD006315; Ependymin; 1.
KW SIGNAL.
FT SIGNAL.
FT
SQ SEQUENCE 1 16 Potential.
234 AA; 26643 MW; D5666FAFB993EDF7 CRC64;

Query Match 43.2%; Score 434.5; DB 2; Length 234;
Best Local Similarity 47.5%; Pred. No. 1.le-34;
Matches 84; Conservative 29; Mismatches 57; Indels 7; Gaps

QY 4 PCQAQQEGRGVMTYQQSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILLYKD 63
DB 30 PCQTAQEQEGRASEWDHWQGRNRRFLISFDGIGMKRVEIEKKSFPGRRFYIEYK 81
QY 64 GYMFQIDQATKQCKWTLTPQWDPLDIPONSTFEDQYSIGGQEQITVQWSDRKARSY 1
DB 90 NKWYTIINNLGCTVSTLKQPNQHTIPSDATLDEYENGDPGSLGNVQWSDRLPARRS 1
QY 124 EFWIGIYTVK---DCYPVQENFTNYS---VILSTRFFDIQLGIKDPVSFTPPSTC 173
DB 150 ESWIGIYTPKTENGCGWPVVEFTDTPDPVSLTRFFDIPIPGIKMNSVFIPPSC 206

RESULT 14
Q6IWN5 BRABE
ID Q6IWN5 BRABE PRELIMINARY; PRT; 194 AA.
AC Q6IWN5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ependymin related protein-1.
OS Branchiostoma belcheri tsingtaunense.
OS Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OC NCBI_TaxID=155462;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Zhang S., Liu Z., Li H., Fan C., Li L., Xu A.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AY616185; AAT39416.1; -; mRNA.
DR

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CC
DR EMBL: AY616185; AAT39416.1; -; mRNA.

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DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; PTHR10697; Ependymin.
DR Pfam; PF00811; Ependymin.
DR PRINTS; PTHR10697; Ependymin.
DR PRINTS; PR00317; Ependymin.
DR PRODOM; PD006315; Ependymin.
DR PRODOM; PD006315; Ependymin.
SQ SEQUENCE 194 AA; 22201 MW; F817321262D30B9A CRC64;

Query Match      28.7%; Score 288; DB 2; Length 194;
Best Local Similarity 36.7%; Pred. No. 3.3e-20;
Matches 65; Conservative 30; Mismatches 70; Indels 12; Gaps 5;

QY 4 PCQAPQWEGQVQMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLY-- 61
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 22 PCSAPPLWEARVSRFDPKRFSEARMSYDSTNRVRRIEENLLE--QRDF-YDVLVIH 78

QY 62 --KDGUMFOIDQATKQCKSKMTLTQPDPLIPQNSTFEDQYSIG---GPQEIIVQEW-S 115
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 79 NTEPGTEYRLNLTKCEKEKELSEFPWRAFPVPNFTLGESYIGTGAVPGAGVLTLSN 138

QY 117 RKARSYETWIGIYTVKDCYVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTC 173
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 139 --TFSGDKYFGAYTVGCIPIQIEFYNSNRTGLVSTFXFDVVGISDPXVFIIPREC 193

RESULT 15
Q4TFW4.TETNG
ID Q4TFW4.TETNG PRELIMINARY; PRT; 211 AA.
AC Q4TFW4;
DT 19-JUL-2005, integrated into UniprotKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome undetermined SCAP4156, whole genome shotgun sequence.
GN ORFNames=GSTENG0001425001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Creaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CRAE01004156; CAF88218.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
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DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin.
DR Pfam; PF00811; Ependymin.
DR PRINTS; PTHR10697; Ependymin.
DR PRINTS; PR00317; Ependymin.
DR PRODOM; PD006315; Ependymin.
DR PRODOM; PD006315; Ependymin.
SQ SEQUENCE 211 AA; 23313 MW; 61340D6A0AAA7B96 CRC64;
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Query Match      18.5%; Score 186; DB 2; Length 211;
Best Local Similarity 28.7%; Pred. No. 5.3e-10;
Matches 51; Conservative 30; Mismatches 85; Indels 12; Gaps 5;

QY 2 PRCPQAPQWEGQVQMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLP--EYIL 59
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 19 PRVCTSPPELTGQLTVSTQNEKVMFAKYKYDALGKRFRIEQG---VYANKSFIDVLL 75

QY 60 LYKDGUMFOIDQATKQCKSKMTLTQPDPLIPQNSTFEDQYSIG---GPQEIIVQEW-S 115
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 76 LYRKGVMYEIDRKNRTCKSKPLKTDFHPLAIPKDANLLGQAILGSSSGWGQGLLVNTW 135

QY 116 DRKSARSYETWIGIYTVKDCYVQETFTINYSVILSTRFFDIQLGKIDPSVFTPPSTC 173
   ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
Db 136 DLPEGGKY---ISTVTOFGCIPISTAVOTSQFGWILTSFDFNVIGITDNCNLPSPFC 190
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Search completed: June 10, 2006, 03:10:32
Job time : 297 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 10, 2006, 03:10:49 ; Search time 49 Seconds
(without alignments)
334.045 Million cell updates/sec
Title: US-10-733-646-2_COPY_38_224
Perfect score: 1005
Sequence: 1 APRPCAPQWEGQVWYQQ.....TPSTCQMAQLKMSDCSW 187
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Issued Patents AA:*

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2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC Celerra_SIDS3/ptodata/2/iaa/PTCUS COMB.pep.*
6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005	100.0	187	US-09-242-890-1	Sequence 1, Appli
2	1005	100.0	200	US-09-242-890-10	Sequence 10, Appli
3	1005	100.0	224	US-09-229-583A-2	Sequence 2, Appli
4	1005	100.0	224	US-09-242-890-11	Sequence 11, Appli
5	1005	100.0	224	US-10-187-904-2	Sequence 2, Appli
6	886	88.2	190	US-09-242-890-2	Sequence 2, Appli
7	886	88.2	224	US-09-242-890-12	Sequence 12, Appli
8	875	87.1	187	US-09-242-890-3	Sequence 3, Appli
9	875	87.1	224	US-09-242-890-13	Sequence 13, Appli
10	201	20.0	39	US-09-242-890-8	Sequence 8, Appli
11	180.5	18.0	221	US-09-229-583A-4	Sequence 4, Appli
12	180.5	18.0	221	US-10-187-904-4	Sequence 4, Appli
13	175	17.4	32	US-09-242-890-5	Sequence 5, Appli
14	163	16.2	215	US-09-229-583A-5	Sequence 5, Appli
15	163	16.2	215	US-10-187-904-5	Sequence 5, Appli
16	162	16.1	212	US-09-229-583A-7	Sequence 7, Appli
17	162	16.1	212	US-10-187-904-7	Sequence 7, Appli
18	151	15.0	217	US-09-229-583A-6	Sequence 6, Appli
19	151	15.0	217	US-10-187-904-6	Sequence 6, Appli
20	148	14.7	216	US-09-229-583A-3	Sequence 3, Appli
21	148	14.7	216	US-10-187-904-3	Sequence 3, Appli
22	147	14.6	26	US-09-242-890-9	Sequence 9, Appli
23	143	14.2	25	US-09-242-890-6	Sequence 6, Appli
24	93	9.3	17	US-09-242-890-7	Sequence 7, Appli
25	82	8.2	419	US-09-134-001C-4658	Sequence 4658, Ap
26	79.5	7.9	2548	US-09-172-422-1	Sequence 1, Appli

27	78	7.8	13	2	US-09-242-890-4	Sequence 4, Appli
28	77	7.7	617	2	US-09-614-912-138	Sequence 138, App
29	76	7.6	1296	2	US-09-614-912-140	Sequence 140, App
30	74.5	7.4	615	2	US-08-676-444-44	Sequence 44, Appli
31	74	7.4	263	2	US-09-248-796A-15254	Sequence 15254, A
32	73.5	7.3	710	2	US-09-489-039A-14121	Sequence 14121, A
33	73	7.3	388	2	US-09-489-039A-11478	Sequence 11478, A
34	73	7.3	483	2	US-10-104-047-3911	Sequence 3911, Ap
35	73	7.3	749	2	US-09-328-352-7588	Sequence 7588, Ap
36	71.5	7.1	399	2	US-09-248-796A-18089	Sequence 18089, A
37	70	7.0	227	2	US-09-710-279-2396	Sequence 2396, Ap
38	69	6.9	2291	2	US-09-822-871-2	Sequence 2, Appli
39	68.5	6.8	215	2	US-09-107-433-4726	Sequence 4726, Ap
40	68.5	6.8	371	2	US-09-538-092-630	Sequence 630, App
41	68.5	6.8	481	2	US-09-489-039A-7805	Sequence 7805, App
42	68.5	6.8	495	2	US-10-094-749-2349	Sequence 2349, Ap
43	68	6.8	521	1	US-08-659-251-3	Sequence 3, Appli
44	68	6.8	521	2	US-09-256-490-3	Sequence 3, Appli
45	68	6.8	521	5	PCT-US96-11445-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-242-890-1
; Sequence 1, Application US/09242890.
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-1

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Best Local Similarity	100.0%;	Pred. No.	8.7e-111;	Indels	0;	Gaps	0;
Matches	187;	Conservative	0;	Mismatches	0;		
Qy	1	APRPCAPQWEGQVWYQQSSGRNSRALLSYDGLNORVRVLDERKALIPCKRLFEYILL	60				
Db	1	APRPCAPQWEGQVWYQQSSGRNSRALLSYDGLNORVRVLDERKALIPCKRLFEYILL	60				
Qy	61	YKDGVMFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQEQITVOEWSDRKSA	120				
Db	61	YKDGVMFQIDQATKQCSKMTLTQWDPDLIPQNSTFEDQYSIGGPQEQITVOEWSDRKSA	120				
Qy	121	RSYETWIGITVKDCYPVQETFTINYSVILSTRFDFIQLGKIDPSVTPPTCQMAQLEK	180				
Db	121	RSYETWIGITVKDCYPVQETFTINYSVILSTRFDFIQLGKIDPSVTPPTCQMAQLEK	180				
Qy	181	MSEDCSW	187				
Db	181	MSEDCSW	187				
RESULT 2							

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US-09-242-890-10
; Sequence 10, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-10

Query Match      100.0%; Score 1005; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 9.6e-111;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
Db 14 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 73
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 120
Db 74 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 133
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 180
Db 134 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 193
QY 181 MSEDSCSW 187
Db 194 MSEDSCSW 200

US-09-229-583A-2
; Sequence 2, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-229-583A-2

Query Match      100.0%; Score 1005; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
Db 38 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 120
Db 98 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 157
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 180
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 217
QY 181 MSEDSCSW 187
Db 218 MSEDSCSW 224

US-09-242-890-11
; Sequence 11, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-11

Query Match      100.0%; Score 1005; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-110;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60
Db 38 APRPCAPQOWEGRWYQOSSGRNRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
QY 61 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 120
Db 98 YKGVNMFQIDQATKQCKMTLTQWPDLDPQNSTFEDQYSIGPQEQITVQWSDRKS 157
QY 121 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 180
Db 158 RSYETWIGIYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKIDPSVFTPPSTCMAQLEK 217
QY 181 MSEDSCSW 187
Db 218 MSEDSCSW 224

US-10-187-904-2
; Sequence 2, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403DI
; RESULT 5
US-10-187-904-2
; Sequence 2, Application US/10187904
; Patent No. 6683161
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403DI
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? Patent No.: 681388
? GENERAL INFORMATION:
? APPLICANT: Ogi, Kasuhiro
? APPLICANT: Onda, Haruo
? TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
? FILE REFERENCE: 2417USOP
? CURRENT APPLICATION NUMBER: US/09/242,890
? CURRENT FILING DATE: 1999-02-28
? PRIOR APPLICATION NUMBER: PCT/JP97/03194
? PRIOR FILING DATE: 1997-08-10

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; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mouse
; US-09-242-890-3

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Best Local Similarity 84.9%; Pred. No. 2.2e-95;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy  2  PRPCQAPQWEGRWQVYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFYILLY 61
Db  2  POPCAAPQWEGRWQVLYQQSSGHNRRALVSVDGLNQVRVLDERKALIPCKRLFYILLY 61
Qy  62  KGVMFQIDQATKQCSKMTLTQPDWDLDPQNSTFEDQYSIGGPOEITVOEWSDRKSAR 121
Db  62  KGVMFQIEQATKQCAKIPLVESGWDPLDIPQNSTFEDQYSIGGPOEILVQEWSDRRTAR 121
Qy  122 SYETWIGIYTKDCYPVQETFTINYSVILSTRPFDIQLGKIDPSVFTPPSTCQMAQLEKM 181
Db  122 SYETWIGIYTKDCYPVQETFIRNYTVVMSTRFDDVQLGKIDPSVFTPPSTCQAAQPEKM 181
Qy  182 SEDCS 186
Db  182 SDGCS 186
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RESULT 9
US-09-242-890-13
; Sequence 13, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 13
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mouse
; US-09-242-890-13

Query Match      87.1%; Score 875; DB 2; Length 224;
Best Local Similarity 84.9%; Pred. No. 2.9e-95;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy  2  PRPCQAPQWEGRWQVYQQSSGRNSRALLSYDGLNQVRVLDERKALIPCKRLFYILLY 61
Db  39  POPCAAPQWEGRWQVLYQQSSGHNRRALVSVDGLNQVRVLDERKALIPCKRLFYILLY 98
Qy  62  KGVMFQIDQATKQCSKMTLTQPDWDLDPQNSTFEDQYSIGGPOEITVOEWSDRKSAR 121
Db  99  KGVMFQIEQATKQCAKIPLVESGWDPLDIPQNSTFEDQYSIGGPOEILVQEWSDRRTAR 158
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Qy  122 SYETWIGIYTKDCYPVQETFTINYSVILSTRPFDIQLGKIDPSVFTPPSTCQMAQLEKM 181
Db  159 SYETWIGIYTKDCYPVQETFIRNYTVVMSTRFDDVQLGKIDPSVFTPPSTCQAAQPEKM 218
Qy  182 SEDCS 186
Db  219 SDGCS 223

RESULT 10
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like
; US-09-242-890-8

Query Match      20.0%; Score 201; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  31  SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 69
Db  1  SYDGLNQVRVLDERKALIPCKRLFYILLYKDGVMFQI 39

RESULT 11
US-09-229-583A-4
; Sequence 4, Application US/09229583A
; Patent No. 6489138
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403
; CURRENT APPLICATION NUMBER: US/09/229,583A
; CURRENT FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorphus mykiss
; US-09-229-583A-4

Query Match      18.0%; Score 180.5; DB 2; Length 221;
Best Local Similarity 25.3%; Pred. No. 6e-13;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;
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Qy	2	PRPQAPQWEGROWMYQOOSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILLY	61
Db	26	PQHCTSPNMTGLVTVMALTYGKATGHYSYDSTNKKLRFTESEHMLNKTEHLEDYLMLF	85
Qy	62	KDGYMFOIDQATKCKSKMTLTQPDWPLDIPQNSTFEDQYSIGG---PQEQITVQWSDRK	118
Db	86	EEGVFYDIDMKNQCKKMSLHSHAHLELPAGAAHQVFLGSDTVQEDNIKVNIWMG-S	144
Qy	119	SARSYETWIGITYTKDCVPVQGETFTTINYSVILSTRFFDIQLGIDKPSVFTTPSTCQMAQL	178
Db	145	VAETKGOYSALTTVGECLPL-STFFVSTDSITLLFSNSEWVTEVKAPEMFTLPSFCEAVEL	203
Qy	179	EK 180	
Db	204	EE 205	
RESULT 12			
US-10-187-904-4			
; Sequence 4, Application US/10187904			
; Patent No. 6683161			
; GENERAL INFORMATION:			
; APPLICANT: Ebner et al.			
; TITLE OF INVENTION: Human Ependymin			
; FILE REFERENCE: PF403D1			
; CURRENT APPLICATION NUMBER: US/10/187,904			
; CURRENT FILING DATE: 2002-07-03			
; PRIOR APPLICATION NUMBER: US 09/229,583			
; PRIOR FILING DATE: 1999-01-13			
; PRIOR APPLICATION NUMBER: US 60/071,330			
; PRIOR FILING DATE: 1998-01-14			
; PRIOR APPLICATION NUMBER: US 60/075,278			
; PRIOR FILING DATE: 1998-02-19			
; NUMBER OF SEQ ID NOS: 20			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 221			
; TYPE: PRT			
; ORGANISM: Oncorhynchus mykiss			
US-10-187-904-4			
Query Match 18.0%; Score 180.5; DB 2; Length 221;			
Best Local Similarity 25.3%; Pred. No. 6e-13;			
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3			
Qy	2	PRPQAPQWEGROWMYQOOSGRNRALLSYDGLNQRVRLDERKALIPCKELFEYILLY	61
Db	26	PQHCTSPNMTGLVTVMALTYGKATGHYSYDSTNKKLRFTESEHMLNKTEHLEDYLMLF	85
Qy	62	KDGYMFOIDQATKCKSKMTLTQPDWPLDIPQNSTFEDQYSIGG---PQEQITVQWSDRK	118
Db	86	EEGVFYDIDMKNQCKKMSLHSHAHLELPAGAAHQVFLGSDTVQEDNIKVNIWMG-S	144
Qy	119	SARSYETWIGITYTKDCVPVQGETFTTINYSVILSTRFFDIQLGIDKPSVFTTPSTCQMAQL	178
Db	145	VAETKGOYSALTTVGECLPL-STFFVSTDSITLLFSNSEWVTEVKAPEMFTLPSFCEAVEL	203
Qy	179	EK 180	
Db	204	EE 205	
RESULT 13			
US-09-242-890-5			
; Sequence 5, Application US/09242890			
; Patent No. 6613887			
; GENERAL INFORMATION:			
; APPLICANT: Ogi, Kasuhiro			
; APPLICANT: Onda, Haruo			
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE			
; FILE REFERENCE: 2417USOP			
; CURRENT APPLICATION NUMBER: US/09/242,890			

Search completed: June 10, 2006, 03:12:14
Job time : 50 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:11:35 ; Search time 181 Seconds
(without alignments)
478.570 Million cell updates/sec

Title: US-10-733-646-2_COPY_38_224

Perfect score: 1005

Sequence: 1 APRCQAPQWEGRVYQQ.....TPPSTCQMAQLEKMSDCSW 187

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA_Main.*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1005	100.0	224	4	US-10-612-788-11
4	1005	100.0	224	4	US-10-733-646-2
5	1005	100.0	224	5	US-10-733-646-2
6	886	88.2	190	4	US-10-612-788-2
7	886	88.2	224	4	US-10-612-788-12
8	875	87.1	187	4	US-10-612-788-3
9	875	87.1	224	4	US-10-612-788-13
10	201	20.0	39	4	US-10-612-788-8
11	180.5	18.0	221	4	US-10-733-646-4
12	180.5	18.0	221	5	US-10-733-646-4
13	175	17.4	32	4	US-10-612-788-5
14	163	16.2	215	4	US-10-733-646-5
15	163	16.2	215	5	US-10-733-646-5
16	162	16.1	212	4	US-10-733-646-7
17	162	16.1	212	5	US-10-733-646-7
18	151	15.0	217	4	US-10-733-646-6
19	151	15.0	217	5	US-10-733-646-6
20	148	14.7	216	4	US-10-733-646-3
21	148	14.7	216	5	US-10-733-646-3
22	147	14.6	26	4	US-10-612-788-9
23	143	14.2	25	4	US-10-612-788-6
24	93	9.3	17	4	US-10-612-788-7
25	82	8.1	419	4	US-10-724-972A-5096
26	81	8.1	970	4	US-10-351-157-135
27	81	8.1	970	4	US-10-352-554-120

28	79.5	7.9	2548	3	US-09-851-682A-1	Sequence 1, Appli
29	79	7.9	144	4	US-10-282-122A-71270	Sequence 71270, A
30	78	7.8	13	4	US-10-612-788-4	Sequence 4, Appli
31	78	7.8	1527	4	US-10-437-421-23	Sequence 23, Appli
32	77	7.7	469	4	US-10-166-349-7	Sequence 7, Appli
33	76.5	7.6	405	4	US-10-424-599-229122	Sequence 229122,
34	76.5	7.6	405	6	US-11-188-298-22061	Sequence 22061, A
35	76.5	7.6	896	4	US-10-408-765A-1811	Sequence 1811, Ap
36	76.5	7.6	923	4	US-10-258-106-7	Sequence 7, Appli
37	76.5	7.6	950	5	US-10-501-035-357	Sequence 357, App
38	76	7.6	1148	3	US-09-949-029-128	Sequence 128, App
39	76	7.6	1148	6	US-11-097-143-9816	Sequence 9816, Ap
40	76	7.6	1302	5	US-10-732-923-1706	Sequence 1706, Ap
41	76	7.6	1431	5	US-10-732-923-1687	Sequence 1687, Ap
42	76	7.6	1490	6	US-11-188-238-4123	Sequence 4123, Ap
43	76	7.6	1500	5	US-10-732-923-1638	Sequence 1638, Ap
44	75.5	7.5	104	4	US-10-437-963-159569	Sequence 159569,
45	75.5	7.5	439	6	US-11-096-568A-30803	Sequence 30803, A

ALIGNMENTS

RESULT 1
US-10-612-788-1
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-788-1

Query Match	100.0%	Score 1005;	DB 4;	Length 187;
Best Local Similarity	100.0%;	Pred. No. 8.7e-101;		
Matches 187;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	APRPCQAPQWEGRVYQQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL	60	
Db	1	APRPCQAPQWEGRVYQQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILL	60	
Qy	61	YKDGWFMIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPOEQTIVQWSDRKS	120	
Db	61	YKDGWFMIDQATKQCSKMTLTQPWDLPDIPQNSTFEDQYSIGGPOEQTIVQWSDRKS	120	
Qy	121	RSVETWIGITVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPFSVFTPPSTCQMAOLEK	180	
Db	121	RSVETWIGITVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPFSVFTPPSTCQMAOLEK	180	
Qy	181	MSEDCSW 187		
Db	181	MSEDCSW 187		

RESULT 2

US-10-612-788-10
; Sequence 10, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro


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; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 1005; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.1e-100;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APRCPAQWEGRGVQMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILL 60
Db 38 APRCPAQWEGRGVQMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILL 97

Qy 61 YKGVWFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 120
Db 98 YKGVWFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKS 157

Qy 121 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEK 180
Db 158 RSYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEK 217

Qy 181 MSEDCSW 187
Db 218 MSEDCSW 224

RESULT 6
US-10-612-788-2
; Sequence 2, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependym-in-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-2

Query Match      88.2%; Score 886; DB 4; Length 190;
Best Local Similarity 86.5%; Pred. No. 8e-88;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRGVQMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILL 61
Db 5 POPCPAQWEGRGVLYQQSSGHNSRALVSDGLNQVRVLDERKALIPCKRLFEYILL 64

Qy 62 KGVWFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 121
Db 65 KGVWFQIEQATKLCAPLAEPWDPDLIPQNSTFEDQYSIGGPQEQIMVQWSDRRTAR 124

Qy 122 SYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKM 181
Db 125 SYETWIGVYAKDCYPVQETFIRNYTVLVSTRFFDVQLGIKDPVSFTPPSTCQTAQPEKM 184

Qy 182 SEDCS 186
Db 185 KENCS 189
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RESULT 7
US-10-612-788-12
; Sequence 12, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependym-in-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-12

Query Match      88.2%; Score 886; DB 4; Length 224;
Best Local Similarity 86.5%; Pred. No. 1e-87;
Matches 160; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRGVQMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILL 61
Db 39 POPCPAQWEGRGVLYQQSSGHNSRALVSDGLNQVRVLDERKALIPCKRLFEYILL 98

Qy 62 KGVWFQIDQATKQCSKMTLTQPWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR 121
Db 99 KGVWFQIEQATKLCAPLAEPWDPDLIPQNSTFEDQYSIGGPQEQIMVQWSDRRTAR 158

Qy 122 SYETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQLGIKDPVSFTPPSTCQMAQLEKM 181
Db 159 SYETWIGVYAKDCYPVQETFIRNYTVLVSTRFFDVQLGIKDPVSFTPPSTCQTAQPEKM 218

Qy 182 SEDCS 186
Db 219 KENCS 223

RESULT 8
US-10-612-788-3
; Sequence 3, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependym-in-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: mouse
US-10-612-788-3

Query Match      87.1%; Score 875; DB 4; Length 187;
Best Local Similarity 84.9%; Pred. No. 1.2e-86;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy 2 PRCPAQWEGRGVQMYQQSSGRNRALLSYDGLNQVRVLDERKALIPCKRLFEYILL 61
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Db 2 POPCPAQWEGRQVLYQSSGHNRRALSYDGLNQRVRLDERKALIPCKRLFYILLY 61
QY 62 KDGVMFQIDQATKQCSKMTLTQPDLDIPONSTFFEDQYSIGGPQEQITVQWSDRSAR 121
Db 62 KEGVMFQIEQATKQCAKIPLVESWDPLDIPONSTFFEDQYSIGGPQEQILVQWSDRRTAR 121
QY 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPVSFTPPSTCQMAQLEKM 181
Db 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPVSFTPPSTCQMAQPEKM 181
QY 182 SEDCS 186
Db 182 SDGCS 186

RESULT 9
US-10-612-788-13
; Sequence 13, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mouse
US-10-612-788-13

Query Match 87.1%; Score 875; DB 4; Length 224;
Best Local Similarity 84.9%; Pred. No. 1.6e-86;
Matches 157; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
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QY 62 KDGVMFQIDQATKQCSKMTLTQPDLDIPONSTFFEDQYSIGGPQEQITVQWSDRSAR 121
Db 99 KEGVMFQIEQATKQCAKIPLVESWDPLDIPONSTFFEDQYSIGGPQEQILVQWSDRRTAR 158
QY 122 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPVSFTPPSTCQMAQLEKM 181
Db 159 SYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPVSFTPPSTCQMAQPEKM 218
QY 182 SEDCS 186
Db 219 SDGCS 223

RESULT 10
US-10-612-788-8
; Sequence 8, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-8
Query Match 20.0%; Score 201; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 SYDGLNQRVRLDERKALIPCKRLFYILLYKDGVMFQI 39

RESULT 11
US-10-733-646-4
; Sequence 4, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Oncomorhynchus mykiss
US-10-733-646-4
Query Match 18.0%; Score 180.5; DB 4; Length 221;
Best Local Similarity 25.3%; Pred. No. 6.1e-11;
Matches 46; Conservative 38; Mismatches 93; Indels 5; Gaps 3;

QY 2 PRCPAQWEGRQVLYQSSGHNRRALSYDGLNQRVRLDERKALIPCKRLFYILLY 61
Db 26 PQHCTSPNMTGVLTVMALTGGEIKATGCHYSYDSTNKKLRFTESEMHJNKTEHLEDYLMLF 85
QY 62 KDGVMFQIDQATKQCSKMTLTQPDLDIPONSTFFEDQYSIGG---PQEQITVQWSDRK 118
Db 86 EGVFYDIDMKNQSCCKNLSHSHALELPAGAAHQVELFLGSDTVQEDNIKNINWG-S 144
QY 119 SARSYETWIGYTVKDCYPVQETFTTINYSVILSTRFFDIQLGKDPVSFTPPSTCQMAQL 178
Db 145 VAETKQYSALTIVGECPLP-STFYSTDSTITLFSNSVTEVVKAPMFTLPSFCEAVEL 203
QY 179 EK 180
Db 204 EE 205

RESULT 12
US-10-733-646-4
; Sequence 4, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:12:30 ; Search time 17 Seconds
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Title: US-10-733-646-2_COPY_38_224

Perfect score: 1005

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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Database :

Published Applications AA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pdb:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pdb:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pdb:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pdb:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pdb:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pdb:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84.5	8.4	931	6 US-10-524-979-2	Sequence 2, Appli
2	69.5	6.9	413	6 US-10-953-349-24222	Sequence 24222, A
3	69.5	6.9	429	6 US-10-953-349-24221	Sequence 24221, A
4	69.5	6.9	431	6 US-10-953-349-24220	Sequence 24220, A
5	69.5	6.9	3882	6 US-10-953-349-5549	Sequence 5549, Ap
6	69.5	6.9	3978	6 US-10-953-349-5548	Sequence 5548, Ap
7	69.5	6.9	4118	6 US-10-953-349-5547	Sequence 5547, Ap
8	69	6.9	802	7 US-11-293-697-3610	Sequence 3610, Ap
9	67.5	6.7	294	6 US-10-953-349-5105	Sequence 5105, Ap
10	67.5	6.7	383	6 US-10-953-349-5104	Sequence 5104, Ap
11	67.5	6.7	439	6 US-10-953-349-5103	Sequence 5103, Ap
12	67.5	6.7	585	7 US-11-293-697-4164	Sequence 4164, Ap
13	66.5	6.6	790	7 US-11-318-939-13	Sequence 13, Appl
14	66	6.6	184	6 US-10-953-349-28907	Sequence 28907, A
15	66	6.6	208	6 US-10-953-349-28906	Sequence 28906, A
16	66	6.6	272	6 US-10-953-349-28905	Sequence 28905, A
17	66	6.6	730	6 US-10-505-928-841	Sequence 841, App
18	65.5	6.5	1871	6 US-10-501-834-26	Sequence 26, Appl
19	65	6.5	695	7 US-11-293-697-4190	Sequence 4190, Ap
20	64.5	6.4	911	7 US-11-313-450-25	Sequence 25, Appl
21	64	6.4	274	7 US-11-293-697-4076	Sequence 4076, Ap
22	64	6.4	362	7 US-11-293-697-2645	Sequence 2645, Ap
23	63.5	6.3	453	6 US-10-471-571A-1056	Sequence 1056, Ap
24	63	6.3	847	6 US-10-505-928-495	Sequence 495, App
25	62.5	6.2	208	6 US-10-953-349-30987	Sequence 30987, A

26	62.5	6.2	244	6 US-10-953-349-30986	Sequence 30986, A
27	62.5	6.2	293	6 US-10-953-349-19396	Sequence 19396, A
28	62.5	6.2	324	6 US-10-953-349-19395	Sequence 19395, A
29	62.5	6.2	359	6 US-10-953-349-19394	Sequence 19394, A
30	62.5	6.2	418	6 US-10-471-571A-4000	Sequence 4000, Ap
31	62.5	6.2	532	6 US-10-471-571A-3482	Sequence 3482, Ap
32	62	6.2	174	6 US-10-953-349-4320	Sequence 4320, Ap
33	62	6.2	277	6 US-10-953-349-4319	Sequence 4319, Ap
34	62	6.2	286	6 US-10-953-349-4318	Sequence 4318, Ap
35	62	6.2	1676	7 US-11-318-227-102	Sequence 102, App
36	61.5	6.1	699	7 US-11-293-697-3395	Sequence 3395, Ap
37	61.5	6.1	700	6 US-10-505-928-351	Sequence 351, App
38	61.5	6.1	1024	7 US-11-121-154-201	Sequence 201, App
39	61	6.1	360	6 US-10-953-349-10497	Sequence 10497, A
40	61	6.1	371	6 US-10-953-349-11789	Sequence 11789, A
41	61	6.1	400	6 US-10-471-571A-4648	Sequence 4648, Ap
42	61	6.1	404	6 US-10-953-349-11788	Sequence 11788, A
43	61	6.1	409	6 US-10-953-349-11787	Sequence 11787, A
44	61	6.1	535	6 US-10-953-349-37802	Sequence 37802, A
45	61	6.1	538	6 US-10-953-349-37801	Sequence 37801, A

ALIGNMENTS

RESULT 1
US-10-524-979-2
; Sequence 2, Application US/10524979
; Publication No. US20060094013A1
; GENERAL INFORMATION:
; APPLICANT: Takemori, Hiroshi
; TITLE OF INVENTION: SALT-INDUCIBLE KINASE 2 AND USE THEREOF
; FILE REFERENCE: WATA-003
; CURRENT APPLICATION NUMBER: US/10/524,979
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 2002-240092
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 2003-23295
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-524-979-2

Query Match	8.4%	Score 84.5;	DB 6;	Length 931;
Best Local Similarity	22.9%	Pred. No. 0.62;		
Matches	57;	Conservative	33;	Mismatches 80;
Indels	79;	Gaps	14;	
Qy	4	PCQAPQWEGRQ-----	-----VMYQSSGSRNALLSYDG-----	LNQRVRLDER 45
Db	181	PYAAPVEFGQYEGPQDLINSMGVLYLVLCG-----	-----ALPDPGPTLPILRQRLV-----	EG 232
Qy	46	KALIP-----	-----CKELFEVILLYKGVMPQIDQATKQCSKMTLTQPWD-PLDIPQNSTPED	98
Db	233	RFRIPYFMSEDCHEILRRMLVLDPSKRLSIAQ-KEHKWMLIEVPVQRPILYPQSQ--	-----EN	289
Qy	99	QYSIGGGPQEQ-----	-----ITVQWSDRSKRSARYETWIGYTV-----	-----KDCYPVQST 141
Db	290	EPSIGEFNEQVLRMLHSLGIDQKTVESLQNSYNHFAIIFLLVERLKSHRSSFPVEQR	-----	349
Qy	142	F-----	-----TTNYSVILSTRFFDIQLGKIDPSV-----	-----FT-PPSTCQMA 176
Db	350	LDGRQRPRSTIAEQTVAKAQTVGLPVTILHPNPNVRLMRSTLLPQASNVFAFSPTSSCQ-A	-----	408
Qy	177	QLEKMSDC 185		
Db	409	EAAPMEBEC 417		

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RESULT 2
US-10-953-349-24222
; Sequence 24222, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24222
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24222
Query Match 6.9%; Score 69.5; DB 6; Length 413;
Best Local Similarity 21.1%; Pred. No. 8;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQVRVLDERKALIPCKRLFEYILLY 61
Db 38 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAAEVRLGMDFAEY 97

Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQOITVQWMSDRKSA 120
Db 98 KTSLSLFQNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 140

Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPS-----VF 167
Db 141 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 199

Qy 168 TPESTCQMAQ 177
Db 200 VGINNCQTVQ 209

RESULT 3
US-10-953-349-24221
; Sequence 24221, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24221
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24221
Query Match 6.9%; Score 69.5; DB 6; Length 429;
Best Local Similarity 21.1%; Pred. No. 8.4;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQVRVLDERKALIPCKRLFEYILLY 61
Db 54 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAAEVRLGMDFAEY 113

Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQOITVQWMSDRKSA 120
Db 114 KTSLSLFQNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 156

Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPS-----VF 167
Db 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPS-----VF 167
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Db 157 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 215
Qy 168 TPESTCQMAQ 177
Db 216 VGINNCQTVQ 225

RESULT 4
US-10-953-349-24220
; Sequence 24220, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24220
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24220
Query Match 6.9%; Score 69.5; DB 6; Length 431;
Best Local Similarity 21.1%; Pred. No. 8.4;
Matches 40; Conservative 33; Mismatches 74; Indels 43; Gaps 8;

Qy 13 GROWMYQSSGRNSRALLSY-----DGLNQVRVLDERKALIPCKRLFEYILLY 61
Db 56 GGOVIYSGPLGRNSHKIVEFEAIPGVPKIKEMYNPATWMLLEVSSVAAEVRLGMDFAEY 115

Qy 62 KDGVMFOIDQA-TKQCSKMTLTQPDWPLDIPQNSTFEDQYSIGGPQOITVQWMSDRKSA 120
Db 116 KTSLSLFQNKALVKELS-----TPPGATDL-----YFPTKYS-----QSTLGQF---KSC 158

Qy 121 RSYETWIGIYTVKDCYPVQETFTINYSVILSTRFFDIQLGKIDPS-----VF 167
Db 159 -FWKQWLTWYRSPDYNLVRYFFTLACALMIGTVFWRIGKKNRESSADLTMIIGAMYAAVIF 217

Qy 168 TPESTCQMAQ 177
Db 218 VGINNCQTVQ 227

RESULT 5
US-10-953-349-5549
; Sequence 5549, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5549
; LENGTH: 3882
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5549
Query Match 6.9%; Score 69.5; DB 6; Length 3882;
Best Local Similarity 24.1%; Pred. No. 1.3e+02;
Matches 52; Conservative 34; Mismatches 71; Indels 59; Gaps 16;

Qy 1 APRPCQ-APOQWEGRO--VMY--QOSSGRNSR-----ALLSYDGLNQVRVLD-ERKALI 49
Db 2992 SPWPSMLSPQESAGRSQVLFPSQKDSYVSPRIGIAVAARDSVSPGISLLELEKKERI 3051
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Qy	50	P-----CKRLPEYILLYKGVWVFQIDQATK-QCSKMTLTQPW-DPLDIP-----QNST----	95
Db	3052	DVKAFCCKDASYML-----SAVLNMTSDRTKDCDQ-----TEEWINPSDPPKLFQWQSSTRLE	3104
Qy	96	-----PEDQYSI-----GGPOEQITVQWSDRKSARSYETWIGIYTVKDC	135
Db	3105	LLKGYRWSTPFSVSEGTMRVPVPKEDGTDLQLRVQRVRSQTKNSR-YEVIFRPNSISGP	3163
Qy	136	YPVQETFTINYSVILSTRFFDIQLGIKDPVSFTTPS	171
Db	3164	YRIE-----NRSMLPIRYQVE-GVSESQWQFLPN	3193

RESULT 6

US-10-953-349-5548	
Sequence 5548, Application US/10953349	
Publication No. US20060107345A1	
GENERAL INFORMATION:	
APPLICANT: ALEXANDROV, Nikolai et al.	
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES	
TITLE OF INVENTION: ENCODED THERBY	
FILE REFERENCE: 2750-1579PUS2	
CURRENT APPLICATION NUMBER: US/10/953,349	
CURRENT FILING DATE: 2004-09-30	
NUMBER OF SEQ ID NOS: 40252	
SOFTWARE: Patent in version 3.3	
SEQ ID NO 5548	
LENGTH: 3978	
TYPE: PRT	
ORGANISM: Arabidopsis thaliana	
US-10-953-349-5548	

Query Match 6.9%; Score 69.5; DB 6; Length 3978;
 Best Local Similarity 24.1%; Pred. No. 1.3e+02;
 Matches 52; Conservative 34; Mismatches 71; Indels 59; Gaps 16;

Qy	1	APRCQ-APQWEGRQ--VMY--QOSSGNSR-----ALLSYDGLNQVRVLD-ERKALI	49
Db	3088	SPMPSMLSPQBSAGRSQVGLFSPQKDSYVSRIGIAVAARDSYSYSGISLLELEKKERI	3147
Qy	50	P-----CKRLPEYILLYKGVWVFQIDQATK-QCSKMTLTQPW-DPLDIP-----QNST----	95
Db	3148	DVKAFCCKDASYML-----SAVLNMTSDRTKDCDQ-----TEEWINPSDPPKLFQWQSSTRLE	3200
Qy	96	-----PEDQYSI-----GGPOEQITVQWSDRKSARSYETWIGIYTVKDC	135
Db	3201	LLKGYRWSTPFSVSEGTMRVPVPKEDGTDLQLRVQRVRSQTKNSR-YEVIFRPNSISGP	3259
Qy	136	YPVQETFTINYSVILSTRFFDIQLGIKDPVSFTTPS	171
Db	3260	YRIE-----NRSMLPIRYQVE-GVSESQWQFLPN	3289

RESULT 7

US-10-953-349-5547	
Sequence 5547, Application US/10953349	
Publication No. US20060107345A1	
GENERAL INFORMATION:	
APPLICANT: ALEXANDROV, Nikolai et al.	
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES	
TITLE OF INVENTION: ENCODED THERBY	
FILE REFERENCE: 2750-1579PUS2	
CURRENT APPLICATION NUMBER: US/10/953,349	
CURRENT FILING DATE: 2004-09-30	
NUMBER OF SEQ ID NOS: 40252	
SOFTWARE: Patent in version 3.3	
SEQ ID NO 5547	
LENGTH: 4118	
TYPE: PRT	
ORGANISM: Arabidopsis thaliana	
US-10-953-349-5547	

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Query Match 6.7%; Score 67.5; DB 6; Length 294;
Best Local Similarity 19.4%; Pred. No. 8.4;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 46 KVMWGESSMIEAERLLASALEHDSNQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 100
QY 63 -----DGVMFQI-DQATKQC 76
Db 101 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAEVIVNDGIVFPVPEKFCCKC 160
QY 77 SKMTLTQPDWDLIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR--SYETW--IGI-YT 131
Db 161 PPLGTNEAMLFLKQKRNCIPDEHYV---QTLTLMQGLESEMERRTVTYTVNVNVSCTKYE 217
QY 132 VKDCYPVQETFTINYS 147
Db 218 AKSWHPV--TFTLENS 231

RESULT 10
US-10-953-349-5104
; Sequence 5104, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5104
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5104

Query Match 6.7%; Score 67.5; DB 6; Length 383;
Best Local Similarity 19.4%; Pred. No. 12;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 135 KVMWGESSMIEAERLLASALEHDSNQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 189
QY 63 -----DGVMFQI-DQATKQC 76
Db 190 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAEVIVNDGIVFPVPEKFCCKC 249
QY 77 SKMTLTQPDWDLIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR--SYETW--IGI-YT 131
Db 250 PPLGTNEAMLFLKQKRNCIPDEHYV---QTLTLMQGLESEMERRTVTYTVNVNVSCTKYE 306
QY 132 VKDCYPVQETFTINYS 147
Db 307 AKSWHPV--TFTLENS 320

RESULT 11
US-10-953-349-5103
; Sequence 5103, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5103
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5103

Query Match 6.7%; Score 67.5; DB 6; Length 439;
Best Local Similarity 19.4%; Pred. No. 14;
Matches 38; Conservative 28; Mismatches 57; Indels 73; Gaps 9;

QY 15 QVMYQSSGRNRALLSYDGL-----NORVRVLDERKALIPCKRLFEYILLYK----- 62
Db 191 KVMWGESSMIEAERLLASALEHDSNQRFVLLSDR-----CAPLYDFGIYKYLLISSPRS 245
QY 63 -----DGVMFQI-DQATKQC 76
Db 246 FVDSFLHTKETRYSVKMSVPIPEEKWRKGSQWIALIRSHAEVIVNDGIVFPVPEKFCCKC 305
QY 77 SKMTLTQPDWDLIPQNSTFEDQYSIGGPQEQITVQWSDRKSAR--SYETW--IGI-YT 131
Db 306 PPLGTNEAMLFLKQKRNCIPDEHYV---QTLTLMQGLESEMERRTVTYTVNVNVSCTKYE 362
QY 132 VKDCYPVQETFTINYS 147
Db 363 AKSWHPV--TFTLENS 376

RESULT 12
US-11-293-697-4164
; Sequence 4164, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4164
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4164

Query Match 6.7%; Score 67.5; DB 7; Length 585;
Best Local Similarity 20.0%; Pred. No. 20;
Matches 30; Conservative 28; Mismatches 51; Indels 41; Gaps 6;

QY 36 NORVRVLDERKALIPCKRLF--EYILLYKDGVMFQIDQATKQCSKMT-----LTQP 84
Db 195 HQTQKIEKPHACIECEQTFLRKSQLIYHENICIQENPGSGQCEKLSRSLVFTKHPKNT 254
QY 85 WDLPLDIPQNSTFEDQYSIGGPQEQITV---QWSDRKSARSYETWIGI----- 129
Db 255 TDKICIP-----NEVRKGSVTKSSLTTHQOHTTEKSYKMCSECGKGTMKRYLIAHQRT 308
QY 130 -----YTVKDCYPVQETFTINYSVILSTR 153
Db 309 HSGEKPYVCKEC---GKGFTVKSNIIVHOR 335

RESULT 13
US-11-318-939-13
; Sequence 13, Application US/11318939
; Publication No. US20060099671A1
; GENERAL INFORMATION:
; APPLICANT: Soff, Gerald
; APPLICANT: Gately, Stephen T.
; APPLICANT: Twardowski, Przemyslaw
```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING ANGIOSTATIN
; FILE REFERENCE: 4228-1-1-1
; CURRENT APPLICATION NUMBER: US/11/318,939
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/09/500,397
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/710,305
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-09-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/991,761
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US97/16539
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-318-939-13

Query Match 6.6%; Score 66.5; DB 7; Length 790;
Best Local Similarity 20.4%; Pred. No. 37;
Matches 49; Conservative 21; Mismatches 95; Indels 75; Gaps 11;

Qy 2 PRCPQAPQWEGROVMYQQSSGRNSRALLSYDGLN---QVRVLDERK-----ALIPCKR 53
Db 241 PR-CTTPPTSGPTYQCLKGRGNGVTVTSAGTCQKWSAQSPHKHNRTPENFPCKN 299

Qy 54 LFEVILLYKGVWFQIDQATKQCSKMTLTQPDPLDIP---QNSTFEDQYSGGPGQBIT 110
Db 300 LEENYCRNPDG-----ETAPWCYTDTSEVRWDYCKIPSCGSSTTSTEHLDPAPVPEQTP 353

Qy 111 VQWSDRKSARSY-----ETWIGIYTVKDCYPVQET-----FTINYSVI 149
Db 354 VAQCYKRGNGESYKGTSTTTTGKCKQSWNSMTHRH-----EKTPGNFPNAGLTWNY--- 406

Qy 150 LSTRFFDIQLGIKDPVSFTP-----PSTCQMAQLKMSDC 185
Db 407 --CRNPAD---KSPWCYTDTDRVRWEYCNLKKCSETEQQVTFNFPATQAQVPSVEDLSEDC 461

RESULT 14
US-10-953-349-28907
; Sequence 28907, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28907
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28907

Query Match 6.6%; Score 66; DB 6; Length 184;
Best Local Similarity 21.8%; Pred. No. 6.7;
Matches 19; Conservative 14; Mismatches 14; Indels 40; Gaps 3;

Qy 8 PQQW-----EGRQV-----MYQQSSGRNSRALLSYDGL----- 35
Db 45 PEKWGGAIELSILSEYVGREIAAYDIQTRCDLYGQGNKYNRAMLIYDGLHYDALAMSP 104

Qy 36 -----NQVRVLDERKALIPCKRL 54
Db 105 AEGAPEEFDQTIYVVDQNRSIGPVEGL 131

RESULT 15
US-10-953-349-28906
; Sequence 28906, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28906
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28906

Query Match 6.6%; Score 66; DB 6; Length 208;
Best Local Similarity 21.8%; Pred. No. 7.8;
Matches 19; Conservative 14; Mismatches 14; Indels 40; Gaps 3;

Qy 8 PQQW-----EGRQV-----MYQQSSGRNSRALLSYDGL----- 35
Db 69 PEKWGGAIELSILSEYVGREIAAYDIQTRCDLYGQGNKYNRAMLIYDGLHYDALAMSP 128

Qy 36 -----NQVRVLDERKALIPCKRL 54
Db 129 AEGAPEEFDQTIYVVDQNRSIGPVEGL 155

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7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	224	100.0	224	AAW51119	Human epe
2	224	100.0	224	AAW51119	Human epe
3	224	100.0	224	AAW51119	Human epe
4	224	100.0	224	AAW51119	Human epe
5	90	40.2	210	ABR40123	Human cel
6	39	17.4	224	AAW51120	Rat epend
7	32	14.3	224	AAW51121	Mouse epe
8	32	14.3	224	AAW51121	Mouse epe
9	8	3.6	8	AAE07249	Peptide #
10	8	3.6	8	AAE07249	Peptide #
11	8	3.6	8	AAE07249	Peptide #
12	8	3.6	8	AAE07249	Peptide #
13	8	3.6	8	AAE07249	Peptide #
14	8	3.6	8	AAE07249	Peptide #
15	8	3.6	8	AAE07249	Peptide #
16	8	3.6	8	AAE07249	Peptide #
17	8	3.6	8	AAE07249	Peptide #
18	8	3.6	8	AAE07249	Peptide #
19	8	3.6	8	AAE07249	Peptide #
20	7	3.1	82	ABY69122	Subsequen
21	7	3.1	82	ABY69122	Subsequen
22	7	3.1	89	ABO74533	Pseudomon
23	7	3.1	125	AAW51119	Human epe

24	7	3.1	131	4	ADM19746	Protein e
25	7	3.1	138	8	ADJ56836	Human AIM
26	7	3.1	140	3	AAB41828	Human ORF
27	7	3.1	140	5	ABG70751	Human apo
28	7	3.1	142	8	ADR96398	Novel S.
29	7	3.1	142	9	AEA60268	Streptoco
30	7	3.1	152	6	ABP75437	Human sec
31	7	3.1	152	9	ADM08553	Human car
32	7	3.1	156	10	AEF39078	Human TNF
33	7	3.1	158	5	ABG32750	Human apo
34	7	3.1	161	8	ADJ56834	Human AIM
35	7	3.1	162	8	ADJ56833	Human AIM
36	7	3.1	167	5	ABG32749	Human apo
37	7	3.1	171	8	ADJ56835	Human AIM
38	7	3.1	172	5	ABG32748	Human apo
39	7	3.1	173	5	ABG32747	Human apo
40	7	3.1	173	8	ADJ56832	Human AIM
41	7	3.1	177	9	ABE06125	Amino aci
42	7	3.1	181	5	ABG32746	Human apo
43	7	3.1	191	6	ABU16476	Protein e
44	7	3.1	196	9	ABM93089	M. xanthu
45	7	3.1	204	4	AAB48942	Human hTL

ALIGNMENTS

RESULT 1

AAW51119	AAW51119 standard; protein; 224 AA.
XX	XX
AC	AAW51119;
XX	XX
DT	06-NOV-1998 (first entry)
XX	XX
DE	Human endymmin-like protein.
XX	XX
KW	Human endymmin-like protein; prophylactic agent; Alzheimer's disease;
KW	Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
KW	dementia; cerebellar degeneration; central nervous system; gliocyte;
KW	memory; neuron.
OS	Homo sapiens.
XX	XX
PH	Location/Qualifiers
FT	Peptide
FT	1. .37
FT	/note= "Signal peptide; This sequence is claimed by the
FT	inventors under claim 10 in the specification"
FT	25. .37
FT	/note= "This sequence represents another signal peptide
FT	which is part of the precursor protein (residues 25-224)
FT	; the precursor protein claimed by the inventors under
FT	claim 9 in the specification"
FT	38. .224
FT	/note= "Human endymmin-like protein; This sequence is
FT	claimed by the inventors under claim 2 in the
FT	specification"
XX	WO9811130-A2.
PN	19-MAR-1998.
XX	XX
PD	10-SEP-1997; 97WO-JP003194.
XX	XX
PR	11-SEP-1996; 96JP-00240880.
PR	28-NOV-1996; 96JP-00318049.
PR	27-MAY-1997; 97JP-00135633.
XX	(TAKE) TAKEDA CHEM IND LTD.
XX	Ogi K, Onda H;
XX	WPI; 1998-250952/22.

CC endodymin activity. Human endodymin can be used to treat conditions in
CC patients having need of the endodymin protein. Conditions that can be
CC treated or detected are nervous system-related disorders, such as
CC Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis,
CC pain, stroke, depression, anxiety, epilepsy and other neurological or
CC psychiatric disorders. Diagnosis of cancers of the nervous system is also
CC included. Endodymin, or its agonists or antagonists may also be used to
CC treat disorders of the blood-brain barrier since endodymin participates
CC in the endothelial cell barrier by modulating cell-matrix interactions.
CC Antagonists may inhibit formation of endodymin-collagen fibrils, which
CC cover endothelial cells of numerous blood vessels, hence anti-endodymin
CC antibodies may regulate angiogenesis

XX SQ Sequence 224 AA;

Query Match 100.0%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 2.5e-216;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPGRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRCPQAPQWEGRVMYQSSG 60
DB 1 MPGRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRCPQAPQWEGRVMYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWTGIVTKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWTGIVTKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGKIDPSTPSTCQMAQLEKMSDSCSW 224
DB 181 INYSVILSTRFFDIQLGKIDPSTPSTCQMAQLEKMSDSCSW 224

RESULT 3

AAAY94654
ID AAY94654 standard; protein; 224 AA.

XX AC AAY94654;

XX DT 29-AUG-2000 (first entry)

XX DE Human homology to endodymin-like protein (HELP) amino acid sequence.

XX KW Homology to endodymin-like protein; HELP; chromosome 7p14-12;
KW central nervous system disorder; peripheral nervous system disorder;
KW Alzheimer's disease; memory loss; stroke; neuronal damage;
KW osteoblast differentiation; proliferation; stimulation; bone wear;
KW arthritis; osteoporosis; cerebral cavernous malformation;
KW Charcot-Marie-Tooth syndrome; human; netrin like protein; NEL.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..37

XX FT Protein /label= Putative signal peptide

XX FT /label= Homology to endodymin-like protein

XX PN WO200032746-A2.

XX PD 08-JUN-2000.

XX PF 30-NOV-1999; 99WO-US028341.

XX PR 30-NOV-1998; 98US-00201442.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Pan Y;

XX XX

DR WPI; 2000-412299/35.
DR N-PSDB; AAA27982.

XX PT New nucleic acid molecules, designated NEL, useful for treating
PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and
PT neuronal damage (e.g. stroke).

XX PS Claim 9; Fig 4; 97pp; English.

XX CC This sequence represents a human homology to endodymin-like protein
CC (HELP) amino acid sequence. Endodymin is a protein that is involved in
CC memory and neuronal regeneration. The human HELP gene is located on
CC chromosome 7p14-12. Northern analysis of HELP expression showed that an
CC approximately 3kb HELP transcript is expressed in the brain, heart, and
CC skeletal muscle. HELP is a secreted protein. Modulators of HELP
CC expression or activity can be used to treat disorders of the central
CC nervous system or peripheral nervous system, e.g. neuronal disorders,
CC memory associated disorders, such as Alzheimer's disease or stroke, or to
CC treat neuronal damage. HELP polypeptides, nucleic acids and modulators of
CC HELP expression or activity may be useful for modulation of osteoblast
CC differentiation, stimulation or proliferation. They may also be used to
CC treat cartilage or bone wearing, arthritis or osteoporosis, disorders
CC such as cerebral cavernous malformation and Charcot-Marie-Tooth disease.
CC The present invention also relates to a secreted protein with homology to
CC netrin, called netrin like protein or NEL. NEL is also referred to as
CC TANGO 205 or T205. Netrin is a chemoattractant. Biological activities of
CC NEL include interacting with the protein encoded by deleted in colorectal
CC cancer, modulation of axon growth, migration and development, modulation
CC of development of the nervous system, and modulation of the guidance of
CC central nervous system commissural axons and peripheral motor axons

XX SQ Sequence 224 AA;

Query Match 100.0%; Score 224; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 2.5e-216;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRCPQAPQWEGRVMYQSSG 60

DB 1 MPGRAPLRTVPGALGAWLLGGLWAWTLGCLSGAVGAPRCPQAPQWEGRVMYQSSG 60

QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQ 120

QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWTGIVTKDCYPVQETFT 180

DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWTGIVTKDCYPVQETFT 180

QY 181 INYSVILSTRFFDIQLGKIDPSTPSTCQMAQLEKMSDSCSW 224

DB 181 INYSVILSTRFFDIQLGKIDPSTPSTCQMAQLEKMSDSCSW 224

RESULT 4

ADY18068

ID ADY18068 standard; protein; 344 AA.

XX AC ADY18068;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 3874.

XX XX

XX XX

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XX XX

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XX XX

```
XX PD 24-FEB-2005.
XX PF
XX PF 11-AUG-2004; 2004WO-US026249.
XX PR
XX PR 11-AUG-2003; 2003US-0493546P.
XX PR
XX (GETH ) GENENTECH INC.
XX PA
XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX WPI; 2005-182330/19.
XX DR
XX PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX PT treating an immune related disorder, e.g. systemic lupus erythematosus,
XX PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX PS Claim 8; SEQ ID NO 3874; 159pp; English.
XX CC The invention relates to an isolated nucleic acid encoding a PRO
XX CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX CC composition, and method are useful for diagnosing and treating an immune
XX CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX CC arthritis. The present sequence represents a PRO polypeptide.
XX SQ Sequence 344 AA;
XX
XX Query Match 100.0%; Score 224; DB 9; Length 344;
XX Best Local Similarity 100.0%; Pred. No. 3.7e-216;
XX Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQVMYQSSG 60
DB 121 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQVMYQSSG 180
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFYFVILLYKDGVMFOIDQATKCKSKMTLTQ 120
DB 181 RNSRALLSYDGLNQRVRLDERKALIPCKRLFYFVILLYKDGVMFOIDQATKCKSKMTLTQ 240
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180
DB 241 PWDPLDIPQNSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 300
QY 181 INYSVILSTRFFDIQGIKDPVSFTPTSTCQMAQLKMSDCSW 224
DB 301 INYSVILSTRFFDIQGIKDPVSFTPTSTCQMAQLKMSDCSW 344
XX
RESULT 5
ABR40123
ID ABR40123 standard; protein; 210 AA.
XX
AC ABR40123;
XX
XX 04-JUL-2003 (first entry)
XX
XX Human cell adhesion and extracellular matrix protein, CADECM-20.
XX
XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
XX KW anticonvulsant; nootropic; neuroprotective; immunosuppressive;
XX KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
XX KW gene therapy; cell adhesion; extracellular matrix; CADECM;
XX KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
XX KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
XX KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
XX KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
XX KW atherosclerosis.
XX
XX Homo sapiens.
XX OS
XX WO2003027230-A2.
XX PN
XX 03-APR-2003.
XX PD
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XX 02-AUG-2002; 2002WO-US024649.
XX PF
XX PF 03-AUG-2001; 2001US-0309964P.
XX PR
XX PR 03-AUG-2001; 2001US-0310119P.
XX PR 17-AUG-2001; 2001US-0313091P.
XX PR 31-AUG-2001; 2001US-0316771P.
XX PR 07-SEP-2001; 2001US-0317896P.
XX PR 21-SEP-2001; 2001US-0324781P.
XX PR 05-OCT-2001; 2001US-0327606P.
XX PR 12-OCT-2001; 2001US-0328960P.
XX PR 09-NOV-2001; 2001US-0344471P.
XX PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
XX Forsythe IJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
XX PI Kallick DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
XX PI Wallia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX WPI; 2003-354645/33.
XX DR N-PSDB; ACC00411.
XX PT New human cell adhesion and extracellular matrix proteins (CADECM),
XX PT useful for diagnosing, treating or preventing disorders associated with
XX PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX PT or stroke.
XX PS Claim 1; Page 203; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX CC and proteins are useful in diagnosing, treating and preventing disorders
XX CC associated with aberrant expression of CADECM, such as immune system
XX CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX CC proliferative disorders (e.g. cancer or atherosclerosis)
XX SQ Sequence 210 AA;
XX
XX Query Match 40.2%; Score 90; DB 6; Length 210;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-81;
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQVMYQSSG 60
DB 121 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQOWEGRQVMYQSSG 180
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKR 90
DB 181 RNSRALLSYDGLNQRVRLDERKALIPCKR 210
XX
XX RESULT 6
XX AAW51120
XX ID AAW51120 standard; protein; 224 AA.
XX
XX AC AAW51120;
XX
XX 06-NOV-1998 (first entry)
XX
XX Rat ependymin-like protein.
XX
XX Rat ependymin-like protein; prophylactic agent; Alzheimer's disease;
XX KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
XX KW dementia; cerebellar degeneration; central nervous system; gliocyte;
XX KW memory; neuron.
XX
XX Rattus sp.
XX OS
```


FH Key Location/Qualifiers
 FT Peptide 1. .37
 FT /label= Putative signal peptide
 FT Protein 38. .224
 FT /label= Homology to ependymin-like protein
 XX
 PN WO200032746-A2.
 XX
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US028341.
 XX
 PR 30-NOV-1998; 98US-00201442.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Pan Y;
 XX
 DR WPI; 2000-412299/35.
 DR N-PSDB; AAA27983.
 XX
 PT New nucleic acid molecules, designated NEL, useful for treating
 PT neurodegenerative disorders (e.g., Alzheimer's disease), memory loss, and
 PT neuronal damage (e.g. stroke).
 XX
 PS Claim 9; Fig 3; 97pp; English.
 XX
 CC This sequence represents a mouse homology to ependymin-like protein
 CC (HELP) amino acid sequence. Ependymin is a protein that is involved in
 CC memory and neuronal regeneration. HELP is a secreted protein. Northern
 CC analysis of HELP expressed in the brain, heart, and skeletal muscle. HELP is
 CC transcript is expressed in the brain, heart, and skeletal muscle. HELP is
 CC expressed in a punctate manner throughout adult mouse brain, suggesting
 CC that it is expressed by neurons, it is also expressed in the membrane
 CC surrounding the placenta. Modulators of HELP expression or activity can
 CC be used to treat disorders of the central nervous system or peripheral
 CC nervous system, e.g. neuronal disorders, memory associated disorders,
 CC such as Alzheimer's disease or stroke, or to treat neuronal damage. HELP
 CC polypeptides, nucleic acids and modulators of HELP expression or activity
 CC may be useful for modulation of osteoblast differentiation, stimulation
 CC or proliferation. They may also be used to treat cartilage or bone
 CC wearing arthritis or osteoporosis, disorders such as cerebral cavernous
 CC malformation and Charcot-Marie-Tooth disease. The present invention also
 CC relates to a secreted protein with homology to netrin, called netrin like
 CC protein or NEL. NEL is also referred to as TANGO 205 or T205. Netrin is a
 CC chemoattractant. Biological activities of NEL include interacting with
 CC the protein encoded by deleted in colorectal cancer, modulation of axon
 CC growth, migration and development, modulation of development of the
 CC nervous system, and modulation of the guidance of central nervous system
 CC commissural axons and peripheral motor axons
 XX
 SQ Sequence 224 AA;
 Query Match 14.3%; Score 32; DB 3; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 SYDGLNQRVRLDERKALIPCKRLFEVILLYK 99
 |||||||
 DB 68 SYDGLNQRVRLDERKALIPCKRLFEVILLYK 99
 |||||||
 RESULT 9
 AAE07249
 ID AAE07249 standard; peptide; 8 AA.
 XX
 AC AAE07249;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Peptide #14 used for counteracting effects of ROS and free radicals.
 XX
 XX Antioxidative enzyme; catalase; CAT; superoxide dismutase; SOD; therapy;

KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;
 KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;
 KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;
 KW trauma; premature aging; neurodegenerative disease; tardive dyskinesia;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;
 KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;
 KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;
 KW polytraumatic shock; schizophrenia; antiulcer; clozapine; Huntington's disease;
 KW cardiant; cerebroprotective; vulnerary; neurotropic; Huntington's disease;
 KW anticonvulsant; neuroprotective; antiarthritis; antiinflammatory; burn;
 KW cytostatic; leukaemia; ophthalmological; antibacterial;
 KW immunosuppressive.
 XX Synthetic.
 OS
 XX WO200136454-A1.
 PN
 XX 25-MAY-2001.
 PD
 XX 17-NOV-2000; 2000WO-US031764.
 PF
 XX 18-NOV-1999; 99US-0166381P.
 PR
 XX (CERE-) CEREMEDIX INC.
 PA
 XX Shashoua VE;
 PI
 XX WPI; 2001-496512/54.
 DR
 XX Novel peptide compound that up regulates expression of a gene encoding
 XX antioxidant enzymes, used to treat or prevent conditions caused by
 PT undesirable elevation of reactive oxygen species and other free radicals.
 PT
 XX Claim 19; Page 66; 102pp; English.
 PS
 XX The invention relates to peptide compounds and methods for upregulating
 CC expression of a gene encoding an antioxidative enzyme, such as catalase
 CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative
 CC effects of reactive oxygen species (ROS) and other free radicals. The
 CC peptides are used as components of pharmaceuticals and dietary
 CC supplements. The peptides are used to treat or to prevent diseases and
 CC conditions characterized by undesirable elevation of ROS and other free
 CC radicals, to upregulate AP-1 transcription factor gene expression and to
 CC treat pain. The disease or conditions include renal reperfusion damage, and
 CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head
 CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature
 CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,
 CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,
 CC ulcerative colitis, human leukaemia and other cancers characterised by
 CC elevation of ROS or free radicals, age-related elevation of ROS or free
 CC radicals, senility, Down's syndrome, macular degeneration, cataracts,
 CC septic shock, polytraumatic shock, schizophrenia, burn injuries,
 CC epilepsy, radiation and/or drug-induced elevation of ROS and free
 CC radicals, where the drug is a neuroleptic or a drug such as clozapine
 CC defined in the specification and tardive dyskinesia. The present sequence
 CC is a peptide used for counteracting effects of ROS and free radicals
 XX
 SQ Sequence 8 AA;
 Query Match 3.6%; Score 8; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 136 QYSIGGPQ 143
 |||||||
 DB 1 QYSIGGPQ 8
 |||||||
 RESULT 10
 AAE07246
 ID AAE07246 standard; peptide; 8 AA.
 XX

AC AAE07246;
XX
DT 06-NOV-2001 (first entry)
XX
DE Peptide #11 used for counteracting effects of ROS and free radicals.
XX
KW Antioxidative enzymes; catalase; CAT; superoxide dismutase; SOD; therapy;
KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;
KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;
KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;
KW trauma; premature aging; neurodegenerative disease; tardive dyskinesia;
KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;
KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;
KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;
KW polytraumatic shock; schizophrenia; antitumor; clozapine; tranquilliser;
KW cardiant; cerebroprotective; vulnerary; nootropic; Huntington's disease;
KW anticonvulsant; neuroprotective; antiarthritic; antiinflammatory; burn;
KW cytostatic; leukaemia; ophthalmological; antibacterial;
KW immunosuppressive.
XX
OS Synthetic.
XX
PN WO200136454-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031764.
XX
PP 18-NOV-1999; 99US-0166381P.
XX
PR (CERE-) CEREMEDIX INC.
XX
PA Shashoua VE;
XX
PI WPI; 2001-496512/54.
XX
DR Novel peptide compound that up regulates expression of a gene encoding
XX PT antioxidant enzymes, used to treat or prevent conditions caused by
XX PT undesirable elevation of reactive oxygen species and other free radicals.
XX
PS Claim 8; Page 64; 102pp; English.
XX
CC The invention relates to peptide compounds and methods for upregulating
CC expression of a gene encoding an antioxidative enzyme, such as catalase
CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative
CC effects of reactive oxygen species (ROS) and other free radicals. The
CC peptides are used as components of pharmaceuticals and dietary
CC supplements. The peptides are used to treat or to prevent diseases and
CC conditions characterised by undesirable elevation of ROS and other free
CC radicals, to upregulate AP-1 transcription factor gene expression and to
CC treat pain. The disease or conditions include renal reperfusion damage,
CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head
CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature
CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,
CC ulcerative colitis, human leukaemia and other cancers characterised by
CC elevation of ROS or free radicals, age-related elevation of ROS or free
CC radicals, senility, Down's syndrome, macular degeneration, cataracts,
CC septic shock, polytraumatic shock, schizophrenia, burn injuries,
CC epilepsy, radiation and/or drug-induced elevation of ROS and free
CC radicals, where the drug is a neuroleptic or a drug such as clozapine
CC defined in the specification and Tardive dyskinesia. The present sequence
CC is a peptide used for counteracting effects of ROS and free radicals.
CC Note: This sequence SEQ.ID.NO.11 is incorrectly designated as
CC SEQ.ID.NO.12 in the sequence listing
XX
SQ Sequence 8 AA;

Query Match 3.6%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAE07246;
XX
DT 06-NOV-2001 (first entry)
XX
DE Peptide #11 used for counteracting effects of ROS and free radicals.
XX
KW Antioxidative enzymes; catalase; CAT; superoxide dismutase; SOD; therapy;
KW reactive oxygen species; ROS; free radical; dietary supplement; stroke;
KW AP-1 transcription factor; renal reperfusion damage; cerebral ischaemia;
KW myocardial infarction; heart attack; pain; atherosclerosis; neuroleptic;
KW trauma; premature aging; neurodegenerative disease; tardive dyskinesia;
KW Parkinson's disease; amyotrophic lateral sclerosis; Alzheimer's disease;
KW arthritis; inflammatory disease; diabetes; ulcerative colitis; cataract;
KW senility; Down's syndrome; macular degeneration; septic shock; epilepsy;
KW polytraumatic shock; schizophrenia; antitumor; clozapine; tranquilliser;
KW cardiant; cerebroprotective; vulnerary; nootropic; Huntington's disease;
KW anticonvulsant; neuroprotective; antiarthritic; antiinflammatory; burn;
KW cytostatic; leukaemia; ophthalmological; antibacterial;
KW immunosuppressive.
XX
OS Synthetic.
XX
PN WO200136454-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031764.
XX
PP 18-NOV-1999; 99US-0166381P.
XX
PR (CERE-) CEREMEDIX INC.
XX
PA Shashoua VE;
XX
PI WPI; 2001-496512/54.
XX
DR Novel peptide compound that up regulates expression of a gene encoding
XX PT antioxidant enzymes, used to treat or prevent conditions caused by
XX PT undesirable elevation of reactive oxygen species and other free radicals.
XX
PS Claim 8; Page 64; 102pp; English.
XX
CC The invention relates to peptide compounds and methods for upregulating
CC expression of a gene encoding an antioxidative enzyme, such as catalase
CC (CAT) or superoxide dismutase (SOD), to counteract harmful oxidative
CC effects of reactive oxygen species (ROS) and other free radicals. The
CC peptides are used as components of pharmaceuticals and dietary
CC supplements. The peptides are used to treat or to prevent diseases and
CC conditions characterised by undesirable elevation of ROS and other free
CC radicals, to upregulate AP-1 transcription factor gene expression and to
CC treat pain. The disease or conditions include renal reperfusion damage,
CC cerebral ischaemia (stroke), myocardial infarction (heart attack), head
CC trauma, atherosclerosis, brain trauma, oxygen toxicity in premature
CC infants, premature aging, spinal cord trauma, neurodegenerative diseases,
CC Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis,
CC Alzheimer's disease, arthritis and other inflammatory diseases, diabetes,
CC ulcerative colitis, human leukaemia and other cancers characterised by
CC elevation of ROS or free radicals, age-related elevation of ROS or free
CC radicals, senility, Down's syndrome, macular degeneration, cataracts,
CC septic shock, polytraumatic shock, schizophrenia, burn injuries,
CC epilepsy, radiation and/or drug-induced elevation of ROS and free
CC radicals, where the drug is a neuroleptic or a drug such as clozapine
CC defined in the specification and Tardive dyskinesia. The present sequence
CC is a peptide used for counteracting effects of ROS and free radicals.
CC Note: This sequence SEQ.ID.NO.11 is incorrectly designated as
CC SEQ.ID.NO.12 in the sequence listing
XX
SQ Sequence 8 AA;

Query Match 3.6%; Score 8; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 SKMTLTOP 121
Db 1 SKMTLTOP 8

RESULT 11
ADJ59106
ID ADJ59106 standard; peptide; 8 AA.
XX
AC ADJ59106;
XX
DT 06-MAY-2004 (first entry)
XX
DE Peptide useful for up-regulating telomerase expression.
XX
KW Telomerase; vulnerary.
XX
OS Synthetic.
XX
PN WO2003066814-A2.
XX
PD 14-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-US003425.
XX
PP 04-FEB-2002; 2002US-0354423P.
XX
PR (CERE-) CEREMEDIX INC.
XX
PI Adams DS, Shashoua VE;
XX
PI WPI; 2003-748118/70.
XX
DR Upregulating telomerase expression in a eukaryotic cell, tissue or organ
XX PT useful for diagnosing and treating degenerative diseases, trauma, or in
XX PT prolonging the aging process, comprises using peptide compositions.
XX
PS Disclosure; SEQ ID NO 19; 72pp; English.
XX
CC The present sequence is that of a peptide that is used in a method of the
CC invention for up-regulating telomerase expression in a eukaryotic cell,
CC tissue or organ. The method involves contacting the eukaryotic cell,
CC tissue or organ with the peptide in an amount effective to up-regulate
CC telomerase expression. The method may be used in therapeutic and
CC prophylactic treatments, diagnostic protocols, research methods and drug
CC screening procedures, and in particular for treating diseases, trauma and
CC conditions of the ageing process. The method solves the problem of
CC shortening of telomeres and the attendant loss of genetic information
CC from chromosomes during successive cellular divisions.
XX
SQ Sequence 8 AA;

Query Match 3.6%; Score 8; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 QYSIGGPQ 143
Db 1 QYSIGGPQ 8

RESULT 12
ADJ59099
ID ADJ59099 standard; peptide; 8 AA.
XX
AC ADJ59099;
XX
DT 06-MAY-2004 (first entry)
XX
DE Peptide useful for up-regulating telomerase expression.
XX
KW Telomerase; vulnerary.

DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64549.
 XX
 PT New Proportionbacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Example 1; SEQ ID NO 22988; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Proportionbacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 235 AA;

Query Match 3.6%; Score 8; DB 6; Length 235;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 RNSRALLS 68
 |||||
 Db 87 RNSRALLS 94

RESULT 15
 ADD25155
 ID ADD25155 standard; protein; 598 AA.
 XX
 AC ADD25155;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Fertility restorer protein #15.
 XX
 KW fertility restorer protein; male sterile plant; viable pollen production;
 KW selection marker.
 XX
 OS Unidentified.
 XX
 XX WO2003006622-A2.
 XX
 XX 23-JAN-2003.
 XX
 XX 12-JUL-2002; 2002WO-US022217.
 PF
 XX 12-JUL-2001; 2001US-0305026P.
 PR
 PR 13-JUL-2001; 2001US-0305363P.
 PR
 PR 30-JUL-2001; 2001US-0308736P.
 XX

PA (UYMC-) UNIV MCGILL.
 PA (DNAL-) DNA LANDMARKS INC.
 XX
 PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;
 XX WPI; 2003-221734/21.
 DR N-PSDB; ADD25156.
 XX
 XX New nuclear fertility restorer genes, useful for restoring fertility in
 PT cytoplasmic male-sterile plants such as Brassica napus plants, or for
 PT increasing production of viable pollen in a plant.
 XX
 PS Claim 5; SEQ ID NO 29; 191pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of isolated
 CC fertility restorer proteins. The DNA and protein sequences of the
 CC invention are useful for restoring fertility in male sterile plants, such
 CC as Brassica napus plants. The DNA and protein sequences of the invention
 CC are useful for increasing production of viable pollen in a plant. The DNA
 CC and protein sequences are also useful as selection markers to identify
 CC transformed plant cells. The present amino acid sequence represents a
 CC fertility restorer protein of the invention.
 XX
 SQ Sequence 598 AA;

Query Match 3.6%; Score 8; DB 7; Length 598;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PSVFTTPS 208
 |||||
 Db 332 PSVFTTPS 339

Search completed: June 10, 2006, 03:19:11
 Job time : 202 secs

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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:19:30 ; Search time 40 Seconds
(without alignments)
538.814 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPGRAPLRTVPGALGAWLLG.....TPPSTCQMAQLKRWSEDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	4.0	1075	1 RNRZB	DNA-directed RNA p
2	7	3.1	130	2 B72702	hypothetical prote
3	7	3.1	158	2 B84268	hypothetical prote
4	7	3.1	167	2 T33602	hypothetical prote
5	7	3.1	194	2 T26391	hypothetical prote
6	7	3.1	243	2 T19090	hypothetical prote
7	7	3.1	253	2 H83238	probable peptidyl-
8	7	3.1	277	2 D98085	hypothetical prote
9	7	3.1	278	2 E95221	sugar ABC transpor
10	7	3.1	297	2 T27584	hypothetical prote
11	7	3.1	353	2 A89933	Xaa-Pro dipeptidas
12	7	3.1	354	2 D86879	ornithine carbamoy
13	7	3.1	368	2 T44305	probable pyruvate
14	7	3.1	369	2 T51477	glutamine-rich pro
15	7	3.1	381	2 T34692	probable transmemb
16	7	3.1	420	2 G95005	phosphoribosylamin
17	7	3.1	420	2 D97878	phosphoribosylamin
18	7	3.1	432	2 T16639	hypothetical prote
19	7	3.1	437	2 C72213	conserved hypothet
20	7	3.1	506	2 T35261	probable metallopro
21	7	3.1	508	2 C95282	probable ABC trans
22	7	3.1	545	2 AC3101	hypothetical prote
23	7	3.1	545	2 G98185	hypothetical prote
24	7	3.1	598	2 B90589	sugar ABC transpor
25	7	3.1	643	2 A97234	ABC-type transport
26	7	3.1	759	2 B83474	probable type II s
27	7	3.1	810	1 DEECK2	metL bifunctional
28	7	3.1	810	2 A86085	aspartokinase II /
29	7	3.1	810	2 E91237	aspartokinase II /

30	7	3.1	811	2 AB0015	aspartate kinase (
31	7	3.1	873	2 E90581	hypothetical prote
32	7	3.1	974	2 T29545	hypothetical prote
33	7	3.1	1070	2 B86922	probable arabinosy
34	7	3.1	1200	2 T15921	hypothetical prote
35	7	3.1	2733	2 S15760	genome polyprotein
36	6	2.7	28	4 JN0014	GABA(A) receptor a
37	6	2.7	46	2 165268	collagen alpha 1(I
38	6	2.7	54	2 B48834	basic fibroblast g
39	6	2.7	78	2 S17872	translation initia
40	6	2.7	81	1 C70910	hypothetical prote
41	6	2.7	95	2 A56842	transcription fact
42	6	2.7	99	2 G70509	hypothetical prote
43	6	2.7	101	2 C72537	hypothetical prote
44	6	2.7	101	2 G71017	hypothetical prote
45	6	2.7	107	2 S63991	thioredoxin trxA -

ALIGNMENTS

RESULT 1

RNRZB

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - rice chloroplast
C;Species: chloroplast Oryza sativa (rice)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JQ0213; S05093
R;Shimada, H.; Whittier, R.F.; Hiratsuka, J.; Maeda, Y.; Hirai, A.; Sugitara, M.
submitted to JIPID, December 1989
A;Reference number: JQ0200
A;Accession: JQ0213
A;Molecule type: DNA
A;Residues: 1-1075 <SHI>
A;Cross-references: UNIPROT:P12091; UNIPARC:UPI000001346ED
A;Experimental source: cv. Nihonbare
R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kon.
Mol. Gen. Genet. 217, 185-194, 1989
A;Title: The complete sequence of the rice (Oryza sativa) chloroplast genome: intermol
of the cereals.
A;Reference number: S05080; MUID:89364698; PMID:2770692
A;Accession: S05093
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1075 <HIR>
A;Cross-references: UNIPARC:UPI00001346ED; EMBL:X15901; NID:g11957; PIDN:CAA33986.1; P
A;Experimental source: cv. Nihonbare
C;Genetics:
A;Gene: rpoB
A;Map position: CP19214-22441
A;Map position: chloroplast
A;Genome: chloroplast
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 4.0%; Score 9; DB 1; Length 1075;
Best Local Similarity 100.0%; Pred.No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 LDIPQNSTF 133

Db 270 LDIPQNSTF 278

RESULT 2

B72702

hypothetical protein APB1033 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72702
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-130 <KAW>
A;Cross-references: UNIPROT:Q9YD79; UNIPARC:UPI000005DDAF; DBJ:AP0000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1033

Query Match 3.1%; Score 7; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LCGLCSL 33
|||||
Db 100 LCGLCSL 106

RESULT 3
B84268
hypothetical protein Vng1120h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84268
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: B84268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-158 <STO>
A;Cross-references: UNIPROT:Q9HQK3; UNIPARC:UPI00000637FB; GB:AE004437; NID:g10580662; F
C;Genetics:
A;Gene: VNG1120H

Query Match 3.1%; Score 7; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LGAVGAP 39
|||||
Db 131 LGAVGAP 137

RESULT 4
T33602
hypothetical protein E02H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33602
R;Kellen, J.; Kramer, J.; Hawkins, M.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid E02H9.
A;Reference number: Z21375
A;Accession: T33602
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-167 <REL>
A;Cross-references: UNIPROT:Q9TZ96; UNIPARC:UPI000017B8A0; EMBL:AF099915; PIDN:AAC68768.
A;Experimental source: strain Bristol N2; clone E02H9
C;Genetics:
A;Gene: CESP:E02H9.2
A;Map position: 3
A;Introns: 89/2

Query Match 3.1%; Score 7; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GLCSLGA 35
|||||
Db 122 GLCSLGA 128

RESULT 5
T26391
hypothetical protein Y105C5B.o - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26391
R;McMurray, A.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20208
A;Accession: T26391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-194 <WIL>
A;Cross-references: UNIPROT:Q9NAM3; UNIPARC:UPI00001641E1; EMBL:AL110479; PIDN:CAB54363
A;Experimental source: clone Y105C5B
C;Genetics:
A;Gene: CESP:Y105C5B.o
A;Introns: 13/1; 56/3; 155/2

Query Match 3.1%; Score 7; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LIPCKRL 91
|||||
Db 122 LIPCKRL 128

RESULT 6
T19090
hypothetical protein C08F11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19090
R;Matthews, L.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19072
A;Accession: T19090
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-243 <WIL>
A;Cross-references: UNIPROT:O62049; UNIPARC:UPI0000060ECC; EMBL:Z83216; PIDN:CAB05674.1
A;Experimental source: clone C08F11
C;Genetics:
A;Gene: CESP:C08F11.3
A;Map position: 4
A;Introns: 14/2; 80/1; 158/2

Query Match 3.1%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 LFEYILL 97
|||||
Db 149 LFEYILL 155

RESULT 7
H83238
probable peptidyl-prolyl cis-trans isomerase, Fkbp-type PA3262 [imported] - Pseudomonas
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83238
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83238
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <STO>
A;Cross-references: UNIPROT:Q9HYX8; UNIPARC:UPI00000C597F; GB:AE004748; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3262
C;Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKEP-type peptidylprolyl isomerase
Query Match 3.1%; Score 7; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 196 LGIKDPS 202
Db 225 LGIKDPS 231
RESULT 8
D98085
hypothetical protein msmG [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98085
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eick, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:Q8DN10; UNIPARC:UPI00000E36DD; GB:AE007317; PIDN:AAL00513.1;
C;Genetics:
A;Gene: msmG
C;Superfamily: maltose transport protein malG
Query Match 3.1%; Score 7; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 80 DERKALI 86
Db 4 DERKALI 10
RESULT 9
E95221
sugar ABC transporter, permease protein SP1895 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95221
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidrich, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, M.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <KUR>
A;Cross-references: UNIPROT:Q9TNW4; UNIPARC:UPI00000C9CFA; GB:AE005672; PIDN:AAK75966.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1895

C;Superfamily: maltose transport protein malG

Query Match 3.1%; Score 7; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DERKALI 86

Db 5 DERKALI 11

RESULT 10

T27584

hypothetical protein ZC455.9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T27584

R;Lightning, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z20390

A;Accession: T27584

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-297 <WIL>

A;Cross-references: UNIPROT:Q23339; UNIPARC:UPI000007E8AE; EMBL:Z75554; PIDN:CAA99960.1

A;Experimental source: clone ZC455

C;Genetics:

A;Gene: CRSP:ZC455.9

A;Map position: 5

A;Introns: 62/1; 180/3; 211/3; 245/3

Query Match 3.1%; Score 7; DB 2; Length 297;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 ILSTRFF 192

Db 95 ILSTRFF 101

RESULT 11

A89933

Xaa-Pro dipeptidase [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: A89933

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: A89933

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-353 <KUR>

A;Cross-references: UNIPROT:Q9TW4; UNIPARC:UPI00000C7F79; GB:BA000018; PID:gl13701328;

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA1360

C;Superfamily: X-Pro aminopeptidase

Query Match 3.1%; Score 7; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 IDQATKQ 112

Db 56 IDQATKQ 62

RESULT 12

D86879

ornithine carbamoyltransferase (EC 2.1.3.3) [imported] - Lactococcus lactis subsp. lactis
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Dec-2004
C:Accession: D86879
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <STO>
A:Cross-references: UNIPROT:Q9CE14; UNIPARC:UPI000006GB9A; GB:AE005176; PID:gl2725085; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: arcB
C:Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoyltr
C:Keywords: transferase

Query Match 3.1%; Score 7; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 DIQLGIK 199
|||||
DB 92 DIQLGIK 98

RESULT 13
T44305
probable pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1-alpha chain [imported] - Hal
C:Species: Haloferax volcanii
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44305
R:Jolley, K.A.; Maddocks, D.G.; Gyles, S.L.; Sinclair, Z.; Dyal-Smith, M.L.; Hough, D.W
submitted to the EMBL Data Library, May 1998
A:Description: 2-Oxoacid dehydrogenase multienzyme complexes in the halophilic Archaea;
A:Reference number: Z22746
A:Accession: T44305
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-368 <JOL>
A:Cross-references: UNIPROT:Q9Y815; UNIPARC:UPI0000062775; EMBL:AF068743; PIDN:AAD34202.
A:Experimental source: strain WFD11
C:Genetics:
A:Gene: pdhA
C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bir
C:Keywords: oxidoreductase

Query Match 3.1%; Score 7; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 RVRVLDE 81
|||||
DB 11 RVRVLDE 17

RESULT 14
T51477
glutamine-rich protein - Arabidopsis thaliana
N:Alternate names: protein K3M16_80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51477
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; New
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51477
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <SAT>
A:Cross-references: UNIPROT:Q9LF51; UNIPARC:UPI00000A0544; EMBL:AL391150

ornithine carbamoyltransferase (EC 2.1.3.3) [imported] - Lactococcus lactis subsp. lactis
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Dec-2004
C:Accession: D86879
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <STO>
A:Cross-references: UNIPROT:Q9CE14; UNIPARC:UPI000006GB9A; GB:AE005176; PID:gl2725085; F
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: arcB
C:Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoyltr
C:Keywords: transferase

Query Match 3.1%; Score 7; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DERKALI 86
|||||
DB 243 DERKALI 249

RESULT 15
T34692
probable transmembrane transport protein - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34692
R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21553
A:Accession: T34692
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-381 <HAR>
A:Cross-references: UNIPROT:O8CJP5; UNIPARC:UPI000017AE03; EMBL:AL023517; PIDN:CAA18988
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC0EDB:SC1B5.14c

Query Match 3.1%; Score 7; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RTVPGAL 14
|||||
DB 79 RTVPGAL 85

Search completed: June 10, 2006, 03:24:58
Job time : 43 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:15:55 ; Search time 296 Seconds
(without alignments)

700.012 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPGRAPLRTVPGALGAWLLG.....TPPSTCQMALEKWSDECSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	224	100.0	224	1	EPDR1_HUMAN	Q9um22 homo sapien
2	206	92.0	344	1	Q96J80_HUMAN	Q96J80 homo sapien
3	103	46.0	224	2	Q99M77_MOUSE	Q99M77 mus musculu
4	85	37.9	224	1	EPDR1_MACFA	Q99M77 macaca fasc
5	59	26.3	227	2	Q9SK77_MACFA	Q9SK77 macaca fasc
6	54	24.1	227	2	Q9SK54_MACFA	Q9SK54 macaca fasc
7	39	17.4	224	2	Q5X110_RAT	Q5X110 rattus norv
8	33	14.7	224	2	Q9SK56_MACFA	Q9SK56 macaca fasc
9	32	14.3	218	2	Q8BOY1_MOUSE	Q8BOY1 mus musculu
10	32	14.3	224	2	Q8CAI2_MOUSE	Q8CAI2 mus musculu
11	32	14.3	224	2	Q99M71_MOUSE	Q99M71 m mammalian
12	9	4.0	206	2	Q6DH25_BRARE	Q6DH25 brachydanio
13	9	4.0	817	2	Q8DCT9_VIBVU	Q8DCT9 vibrio vuln
14	9	4.0	819	2	Q7MH12_VIBVU	Q7MH12 vibrio vuln
15	9	4.0	1067	2	Q6QXV7_ORYSA	Q6QXV7 oryza sativ
16	9	4.0	1067	2	Q7DNA7_ORYSA	Q7DNA7 oryza sativ
17	9	4.0	1067	2	Q7XW77_ORYSA	Q7XW77 oryza sativ
18	9	4.0	1075	1	RPOB_ORYNI	Q6en14 oryza niyar
19	9	4.0	1075	1	RPOB_ORYSA	P12091 oryza sativ
20	9	4.0	1075	2	Q6QY83_ORYSA	Q6QY83 oryza sativ
21	9	4.0	1143	2	Q4BOM6_BURVI	Q4BOM6 burholderi
22	9	4.0	1427	2	Q339H4_ORYSA	Q339H4 oryza sativ
23	8	3.6	140	2	Q6IIF2_DROME	Q6IIF2 drosophila
24	8	3.6	185	2	Q2N779_9SPHN	Q2N779 erythrobact
25	8	3.6	203	2	Q6WNG6_BRARE	Q6WNG6 branchiost
26	8	3.6	223	2	Q8XNU6_CLOPE	Q8XNU6 clostridium
27	8	3.6	308	2	Q7NNL6_GLOVI	Q7NNL6 gloeobacter
28	8	3.6	420	2	Q410H5_KINRA	Q410H5 kinococcus
29	8	3.6	514	2	Q64BG4_9ARCH	Q64BG4 uncultured
30	8	3.6	536	2	Q4CVM0_TRYCR	Q4CVM0 trypanosoma
31	8	3.6	538	2	Q4D988_TRYCR	Q4D988 trypanosoma

RESULT 1
EPDR1_HUMAN
ID EPDR1_HUMAN STANDARD; PRT; 224 AA.
AC Q9UM22;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2001, sequence version 2.
DT 07-FEB-2006, entry version 40.
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1
DE Protein).
GN Name=EPDR1; Synonyms=MERP1, UCC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TI TISSUE=Cervix;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Harte S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 51-224
RA Nimrich I., Erdmann S., Melchers U.;
RT "Genes that are differentially expressed in colon cancer.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted protein.

32 3.6 774 2 Q746U9 GEOSL Q746U9 geobacter s
33 8 798 2 Q8SUR3 ENCCU Q8SUR3 encephalito
34 8 856 2 Q6AAP2_PROAC Q6AAP2 propionibac
35 8 1198 2 Q3QV23_9RHOB Q3QV23 silicibacte
36 7 85 2 Q67JW5_SYMTH Q67JW5 symbiobacte
37 7 3.1 88 2 Q6LXM0_METMP Q6LXM0 methanococc
38 7 3.1 96 2 Q424Y1_DESHA Q424Y1 desulfitoba
39 7 3.1 109 2 Q4UTN8_XANC8 Q4UTN8 xanthomonas
40 7 3.1 109 2 Q8P9Z7_XANCP Q8P9Z7 xanthomonas
41 7 3.1 113 2 Q4H7B9_9DEIO Q4H7B9 deinoococcus
42 7 3.1 116 2 Q47IP0_DECAR Q47IP0 dechloromon
43 7 3.1 122 2 Q3MVP8_9DELT Q3MVP8 syntrophoba
44 7 3.1 130 2 Q9YD79_AERPE Q9YD79 aeropyrum p
45 7 3.1 130 2 Q8KBE6_CHLTE Q8KBE6 chlorobium

ALIGNMENTS

```
CC -!- SIMILARITY: Belongs to the ependymin family.
CC -----
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CC -----
CC EMBL: AF31252; AAK26441.1; -; Genomic DNA.
CC EMBL: BC000686; AAH00686.2; ALT_INIT; mRNA.
CC EMBL: BC018299; AAH18299.1; -; mRNA.
CC EMBL: AJ250475; CAB60269.1; ALT_INIT; mRNA.
CC EMBL: ENSG00000086289; Homo sapiens.
CC HGNC: HGNC:17572; EPDR1.
CC LinkHub; Q9UM22; -.
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC ProDom; PD006315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; 1.
CC PROSITE; PS00899; EPENDYMIN_2; 1.
CC Glycoprotein; Signal
FT SIGNAL 1 Potential.
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT FTID=PRO_0000008351.
FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CONFLICT 207 207 P -> S (in Ref. 3).
SQ SEQUENCE 224 AA; 25437 MW; 84ADBA3666261611 CRC64;

Query Match 100.0%; Score 224; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 58-226;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPAQPQWEGRWVYQSSG 60
DB 1 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPAQPQWEGRWVYQSSG 60
QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKCKSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKCKSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIOLGKIDPSVFTPTSTCMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIOLGKIDPSVFTPTSTCMAQLEKMSDCSW 224

RESULT 2
Q96J80 HUMAN PRELIMINARY; PRT; 344 AA.
ID Q96J80;
AC Q96J80;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Mammalian ependymin related protein 1.
GN Name=EPDR1; Synonyms=MERP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RA "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635(2001).
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CC -----
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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21940632; PubMed=11943480; DOI=10.1016/S0378-1119(02)00434-1;
RA Gregorio-King C.C., McLeod J.L., Collier F.M., Collier G.R.,
RA Bolton K.A., Van Der Meer G.J., Apostolopoulos J., Kirkland M.A.;
RA "MERP1: a mammalian ependymin-related protein gene differentially
RT expressed in hematopoietic cells.";
RL Gene 286:249-257(2002).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AY027862; AAK15788.2; -; mRNA.
CC Ensembl; ENSG00000086289; Homo sapiens.
CC HGNC; HGNC:17572; EPDR1.
CC LinkHub; Q96J80; -.
CC GO; GO:0005576; C:extracellular region; IEA.
CC GO; GO:0005509; F:calcium ion binding; IEA.
CC GO; GO:0007160; P:cell-matrix adhesion; IEA.
CC InterPro; IPR001299; Ependymin.
CC PANTHER; PTHR10697; Ependymin; 1.
CC PRINTS; PR00317; EPENDYMIN.
CC ProDom; PD006315; Ependymin; 1.
CC PROSITE; PS00898; EPENDYMIN_1; UNKNOWN 1.
SQ SEQUENCE 344 AA; 38141 MW; 34D75B84822692DA CRC64;

Query Match 92.0%; Score 206; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 5.7e-207;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPAQPQWEGRWVYQSSG 60
DB 121 MPRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPAQPQWEGRWVYQSSG 180
QY 61 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKCKSKMTLTQ 120
DB 181 RNSRALLSYDGLNQRVRVLDERKALIPCKRLFEYILLYKDGVMFQIDQATKCKSKMTLTQ 240
QY 121 PWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTKDCYPVQETFT 180
DB 241 PWDPLDIPQNSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTKDCYPVQETFT 300
QY 181 INYSVILSTRFFDIOLGKIDPSVFTPT 206
DB 301 INYSVILSTRFFDIOLGKIDPSVFTPT 326

RESULT 3
Q99M77 MOUSE PRELIMINARY; PRT; 224 AA.
ID Q99M77;
AC Q99M77;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Mammalian ependymin related protein 1.
GN Name=Ucc1; Synonyms=Epdr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/104454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RA "Identification and characterization of a novel family of mammalian
RT ependymin-related proteins (MERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635(2001).
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CC -----
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CC -----
DR EMBL; AY027861; AAK15787.1; -; mRNA.
DR MGI; MGI-2152290; Epdrl.
DR MGI; MGI-2152290; Ucc1.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
SQ SEQUENCE 224 AA; 25437 MW; DB6CA5A9A7289E95 CRC64;

Query Match 46.0%; Score 103; DB 2; Length 224;
Best Local Similarity 99.5%; Pred. No. 4.8e-99;
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 GLAWTLGCLGSLGAVGAPRCQAPQWEGQVQWYQSSGRNSRALLSYDGLNQRVRLD 80
DB 21 GLAWTLGCLGSLGAVGAPRCQAPQWEGQVQWYQSSGRNSRALLSYDGLNQRVRLD 80

QY 81 ERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQVSI 140
DB 81 ERKALIPCKRLFEVILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQVSI 140

QY 141 GPQEQITVQWSDRSKARSYETWIGIYTVKDCVPVQSTFTINYSVILSTRFFDIQLGIKD 200
DB 141 GPQEQITVQWSDRSKARSYETWIGIYTVKDCVPVQSTFTINYSVILSTRFFDIQLGIKD 200

QY 201 PSVFTPPSTCQMAQLKMSDCSW 224
DB 201 PSVFTPPSTCQMAQLKMSDCSW 224

RESULT 4
EPDR1_MACFA
ID EPDR1_MACFA STANDARD; PRT; 224 AA.
AC Q9NOC7;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 21-FEB-2006, entry version 2.
DE Mammalian ependymin-related protein 1 precursor (MERP-1) (UCC1 protein).
GN Name:EPDR1; Synonyms:MERP1, UCC1; ORFNames=QcCE-12983;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Brain cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the ependymin family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB046003; BAB01585.1; ALT_INIT; mRNA.
DR LinkHub; Q9NOC7; -;
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.

DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 37 Potential.
FT CHAIN 38 224 Mammalian ependymin-related protein 1.
FT CARBOHYD 130 130 /FTID=PRO_000008352.
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 224 AA; 25484 MW; 3594311D15AB4BB7 CRC64;

Query Match 37.9%; Score 85; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.8e-80;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 LWAWTLGCLGSLGAVGAPRCQAPQWEGQVQWYQSSGRNSRALLSYDGLNQRVRLD 81
DB 22 LWAWTLGCLGSLGAVGAPRCQAPQWEGQVQWYQSSGRNSRALLSYDGLNQRVRLD 81

QY 82 RKALIPCKRLFEVILLYKDGVMFQI 106
DB 82 RKALIPCKRLFEVILLYKDGVMFQI 106

RESULT 5
Q9SK77_MACFA
ID Q9SK77_MACFA PRELIMINARY; PRT; 227 AA.
AC Q9SK77;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Temporal lobe right;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Medulla oblongata;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes";
RL Gene 275:31-37(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Medulla oblongata;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB063094; BAB60800.1; -; mRNA.
DR EMBL; AB097520; BAC41745.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR ProDom; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1; UNKNOWN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
KW Hypothetical protein.

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.Z., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RC NIH MGC Project;

RG Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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CC -----

CC EMBL: BC083701.1; AAH83701.1; -; mRNA.

DR Ensembl: ENSRNOG0000018989; Rattus norvegicus.

DR GO: GO:0005576; C:extracellular region; IEA.

DR GO: GO:0005509; F:calcium ion binding; IEA.

DR GO: GO:0007160; P:cell-matrix adhesion; IEA.

DR InterPro: IPR001299; Ependymin.

DR PANTHER: PTHR10697; Ependymin; 1.

DR PRINTS: PR00317; EPENDYMIN.

DR ProDom: PD006315; Ependymin; 1.

DR SEQUENCE 224 AA; 25639 MW; B8DE78133B1CB821 CRC64;

SQ

Query Match 17.4%; Score 39; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 7, 1e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLPFYILLYKDGVMFQI 106

|||||

Db 68 SYDGLNQRVRLDERKALIPCKRLPFYILLYKDGVMFQI 106

RESULT 8

Q95K56 MACFA PRELIMINARY; PRT; 218 AA.

ID ID Q95K56 MACFA PRELIMINARY; PRT; 218 AA.

AC AC Q95K56;

DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 15.

DT Hypothetical protein.

DE Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopithecidae; Cercopithecinae; Macaca.

OX NCBI_Taxid=9541;

RNA [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Medulla oblongata;

RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;

RT "Isolation of full-length cDNA clones from macaque brain cDNA

RT libraries.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; AB066535; BAB2211.1; ; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR001299; Ependymin.
DR PANTHER; PTHR10697; Ependymin; 1.
DR PRINTS; PR00317; EPENDYMIN.
DR PRODOM; PD006315; Ependymin; 1.
DR PROSITE; PS00898; EPENDYMIN_1.
DR PROSITE; PS00899; EPENDYMIN_2; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24970 MW; 8B8524C0D986677C CRC64;

Query Match 14.7%; Score 33; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 VQWSDRKSARSYETWGIYTVKDCYPVQETFT 180
Db 142 VQWSDRKSARSYETWGIYTVKDCYPVQETFT 174

RESULT 9
QB0Y1_MOUSE PRELIMINARY; PRT; 224 AA.
AC QB0Y1;
DT 01-MAR-2003, integrated into UniprotKB/TREMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
DE library, clone:B230347119 product:MAMMALIAN EPENDYMIN RELATED PROTEIN-
DE 2 (SIMILAR TO MAMMALIAN EPENDYMIN RELATED PROTEIN 1) homolog.
GN Names:Epd2; Synonyms:AU040950;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Hatanaka M., Hayashizaki Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lacroix L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
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RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Aragawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira T.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the PANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hirokawa T., Kondo S., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaio I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schram L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Watanabe R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Momo H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RN [8]

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
 RA Fujiwara S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]

NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC -----

DR ENBL; AK038733; BAC30113.1; -; mRNA.
 DR Ensembl; ENSMUSG0000002808; Mus musculus.
 DR MGI; MGI:2145369; AU040950.

DR MGI; MGI:2145369; Ecd2.

DR GO; GO:0005615; C:extracellular space; RCA.

DR GO; GO:0005509; F:calcium ion binding; RCA.

DR GO; GO:0007160; P:cell-matrix adhesion; RCA.

DR InterPro; IPR001299; Ependymin.

DR PANTHER; PTHR10697; Ependymin; 1.

DR PRINTS; PR00317; Ependymin.

DR PRODOM; PD006315; Ependymin; 1.

SQ SEQUENCE 224 AA; 25515 MW; D49BAC6C8A4857BB CRC64;

Query Match 14.3%; Score 32; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 SYDGLNQRVRLDERKALIFCKLFEYLLYK 99

|||||

Db 68 SYDGLNQRVRLDERKALIFCKLFEYLLYK 99

RESULT 11

Q99M71_MOUSE PRELIMINARY; PRT; 224 AA.

ID Q99M71_MOUSE

AC Q99M71;

DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 29.

DE Mammalian ependymin related protein-2 (Ependymin 2) (Adult male

DE diencephalon cDNA, RIKEN full-length enriched library,

DE clone:9330154O03 product:mammalian ependymin related protein-2) (Adult

DE male cerebellum cDNA, RIKEN full-length enriched library,

DE clone:1500034M21 product:Mammalian ependymin related protein-2

DE (similar to mammalian ependymin related protein 1), full insert

DE sequence).

GN Name=Epd2; Synonyms=AU040950, MERP2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL6/J, and C57BL/6J;
RX MEDLINE=21622606; PubMed=11749721; DOI=10.1089/10454901753340613;
RA Apostolopoulos J., Sparrow R.L., McLeod J.L., Collier F.M.,
RA Darcy P.K., Slater H.R., Ngu C., Gregorio-King C.C., Kirkland M.A.;
RT "Identification and characterization of a novel family of mammalian
RT spendymin-related proteins (NERPs) in hematopoietic, nonhematopoietic,
RT and malignant tissues.";
RL DNA Cell Biol. 20:625-635 (2001).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX STRAIN=MGC Project;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama T., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Baile T.L.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.B., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottguet-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.C., Pavan W.J., Ring B.Z., Ringwald M.,
RA Rest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tamoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Zimmer A., Zimmer A.,
RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimura N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566 (2005).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=22534683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanagaya A., Kawai H., Kawasawa Y., Kedzieraki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505550;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wshhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [9]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [10]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitaunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [11]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA
RA
Query Match 14.3%; Score 32; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDKALIPCKLFEYILLYK 99
Db |||||||||||||||||||||||||||||||
68 SYDGLNQRVRLDKALIPCKLFEYILLYK 99

RESULT 12
Q6DH25_BRARE PRELIMINARY; PRT; 206 AA.
AC Q6DH25;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Ependymin related protein 1.
GN Name=epdri;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Eye;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Zeehan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Eye;
RC NIH MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC076158; AAH76158.1; -; mRNA.
DR Ensembl; ENSDARG0000045420; Danio rerio.
DR ZFIN; ZDB-GENE-040718-113; epdri.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR010697; Ependymin.
DR PANTHER; PT00317; Ependymin.
DR PRINTS; PR00317; Ependymin.
DR ProDom; PD006315; Ependymin; 1.
SQ SEQUENCE 206 AA; 23467 MW; 64646DEB4506530D CRC64;

Query Match 4.0%; Score 9; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 KDCYPVQET 178
Db |||||||
154 KDCYPVQET 162

RESULT 13
Q8DCT9_VIBVU PRELIMINARY; PRT; 817 AA.
ID Q8DCT9_VIBVU PRELIMINARY; PRT; 817 AA.
AC Q8DCT9;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Exoribonuclease R.
GN OrderedLocNames=VV11304; ORFNames=VV1_1304;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AE016795; AAC09759.1; -; Genomic_DNA.
DR BioCyc; VVU1216895:VV11304-MONOMER; -.
DR GO; GO:0004540; F:ribonuclease activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016070; P:RNA metabolism; IEA.
DR InterPro; IPR011129; CSP.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR013223; RNase_B_OB_N.
DR InterPro; IPR001900; RNase_II_R.
DR InterPro; IPR004476; RNase_II_R_bac.
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DR InterPro; IPR011805; RNase R_bac.
DR InterPro; IPR003029; Sl_RNA_Ed.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00773; RNB; 2.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMS; TIGR00358; 3_prime_RNase; 1.
DR TIGRFAMS; TIGR02063; RNase R; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
DR PROSITE; PS01126; S1; 1.
KW Complete proteome.
SQ SEQUENCE 817 AA; 93124 MW; F33DB28163DDAF83 CRC64;

Query Match 4.0%; Score 9; DB 2; Length 817;
Best Local Similarity 100.0%; Pred.No. 6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRVLDERKA 84
DB 149 VRVLDERKA 157

RESULT 14
Q7MH12_VIBVY PRELIMINARY; PRT; 819 AA.
AC Q7MH12;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Exoribonuclease R.
GN OrderedLocName=VV3061;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Hor H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Chen L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
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-----
DR EMBL; BA000037; BAC95925.1; -; Genomic_DNA.
DR BioCyc; VVUL196600:VV3061-MONOMER; -.
DR GO; GO:0004540; F:ribonuclease activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016070; P:RNA metabolism; IEA.
DR InterPro; IPR011129; CSP.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR InterPro; IPR012323; RNase_B_OB_N.
DR InterPro; IPR001900; RNase_II_R.
DR InterPro; IPR004476; RNase_II_R_bac.
DR InterPro; IPR011805; RNase_R_bac.
DR InterPro; IPR003029; S1_RNA_Ed.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00773; RNB; 2.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00357; CSP; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMS; TIGR00358; 3_prime_RNase; 1.
DR TIGRFAMS; TIGR02063; RNase R; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
DR PROSITE; PS01126; S1; 1.
KW Complete proteome.
SQ SEQUENCE 819 AA; 93342 MW; D52BE95D603D4D26 CRC64;
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Query Match 4.0%; Score 9; DB 2; Length 819;
Best Local Similarity 100.0%; Pred.No. 6.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VRVLDERKA 84
DB 151 VRVLDERKA 159

RESULT 15
Q6QXV7_ORYSA PRELIMINARY; PRT; 1067 AA.
AC Q6QXV7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE RNA polymerase beta chain.
GN Name=rpoB; ORFNames=Nip036, PA036;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15122023; DOI=10.1104/pp.103.031245;
RA Tang J., Xia H., Cao M., Zhang X., Zeng W., Hu S., Tong W., Wang J.,
RA Wang J., Yu J., Yang H., Zhu L.;
RT "A Comparison of Rice Chloroplast Genomes.";
RL Plant Physiol. 135:412-420(2004).
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DR EMBL; AY522331; AAS46174.1; -; Genomic_DNA.
DR EMBL; AY522330; AAS46111.1; -; Genomic_DNA.
DR Gramene; Q6QXV7; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007121; RNA_pol_B.
DR InterPro; IPR007644; RNA_pol_Rpb2_1.
DR InterPro; IPR007642; RNA_pol_Rpb2_2.
DR InterPro; IPR007645; RNA_pol_Rpb2_3.
DR InterPro; IPR007120; RNA_pol_Rpb2_6.
DR InterPro; IPR007641; RNA_pol_Rpb2_7.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
SQ SEQUENCE 1067 AA; 120770 MW; F643A6F524D7CD38 CRC64;
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Query Match 4.0%; Score 9; DB 2; Length 1067;
Best Local Similarity 100.0%; Pred.No. 8.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 LDIPQNSTF 133
DB 262 LDIPQNSTF 270
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Search completed: June 10, 2006, 03:24:12
Job time : 300 secs


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/ APPLICANT: Onda, Haruo
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
/ PRIOR FILING DATE: 1999-02-28
/ PRIOR APPLICATION NUMBER: PCT/JP97/03194
/ PRIOR FILING DATE: 1997-08-10
/ PRIOR APPLICATION NUMBER: JP 8-240880
/ PRIOR FILING DATE: 1996-09-11
/ PRIOR APPLICATION NUMBER: JP 8-318049
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: JP 9-135633
/ PRIOR FILING DATE: 1997-05-27
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE:
/ SEQ ID NO 11
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Human
/ ORGANISM: Homo sapiens
US-09-242-890-11

Query Match 100.0%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-220;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
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RESULT 3
US-10-187-904-2
/ Sequence 2, Application US/10187904
/ Patent No. 6683161
/ GENERAL INFORMATION:
/ APPLICANT: Ebner et al.
/ TITLE OF INVENTION: Human Ependymin
/ FILE REFERENCE: PF403D1
/ CURRENT APPLICATION NUMBER: US/10/187,904
/ CURRENT FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US 09/229,583
/ PRIOR FILING DATE: 1999-01-13
/ PRIOR APPLICATION NUMBER: US 60/071,330
/ PRIOR FILING DATE: 1998-01-14
/ PRIOR APPLICATION NUMBER: US 60/075,278
/ PRIOR FILING DATE: 1998-02-19
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-187-904-2

Query Match 100.0%; Score 224; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-220;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSG 60
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QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQWSDRKSARSYETWIGYITVKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
```

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RESULT 4
US-09-242-890-10
/ Sequence 10, Application US/09242890
/ Patent No. 6613887
/ GENERAL INFORMATION:
/ APPLICANT: Ogi, Kasuhiro
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
/ PRIOR APPLICATION NUMBER: PCT/JP97/03194
/ PRIOR FILING DATE: 1997-08-10
/ PRIOR APPLICATION NUMBER: JP 8-240880
/ PRIOR FILING DATE: 1996-09-11
/ PRIOR APPLICATION NUMBER: JP 8-318049
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: JP 9-135633
/ PRIOR FILING DATE: 1997-05-27
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE:
/ SEQ ID NO 10
/ LENGTH: 200
/ TYPE: PRT
/ ORGANISM: Human
/ ORGANISM: Homo sapiens
US-09-242-890-10
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Query Match 89.3%; Score 200; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.3e-196;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSGRNLRALLSYDGLNQRVRLDERKA 84
DB 1 WTLGCLSLGAVGAPRCPQAPQWEGRWYQQSSGRNLRALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTFEDQYSIGGPQ 144
DB 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPONSTFEDQYSIGGPQ 120
QY 145 QITVQWSDRKSARSYETWIGYITVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 204
DB 121 QITVQWSDRKSARSYETWIGYITVKDCYPVQETFTINYSVILSTRFFDIQLGIKDPSPV 180
QY 205 TPPSTCQMAQLEKMSDCSW 224
DB 181 TPPSTCQMAQLEKMSDCSW 200
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RESULT 5
US-09-242-890-1
/ Sequence 1, Application US/09242890
/ Patent No. 6613887
/ GENERAL INFORMATION:
/ APPLICANT: Ogi, Kasuhiro
/ TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
/ FILE REFERENCE: 2417USOP
/ CURRENT APPLICATION NUMBER: US/09/242,890
/ CURRENT FILING DATE: 1999-02-28
```

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; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-1

Query Match      83.5%; Score 187; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 7.6e-183;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 APPCPAQWEGROVMYQSSGRNRRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 97
Db 1 APPCPAQWEGROVMYQSSGRNRRALLSYDGLNQRVRLDERKALIPCKRLFEYILL 60

QY 98 YKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGPQEQITVQWSDRKS 157
Db 61 YKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGPQEQITVQWSDRKS 120

QY 158 RSVETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQGIKDPSPVTPSTCMAQLEK 217
Db 121 RSVETWIGIYTKDCYPVQETFTINYSVILSTRFFDIQGIKDPSPVTPSTCMAQLEK 180

QY 218 MSDEDCSW 224
Db 181 MSDEDCSW 187

RESULT 6
US-09-242-890-8
; Sequence 8, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like P
US-09-242-890-8

Query Match      17.4%; Score 39; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.4e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 1 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 39
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RESULT 7
US-09-242-890-2
; Sequence 2, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-2

Query Match      17.4%; Score 39; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 34 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 72

RESULT 8
US-09-242-890-12
; Sequence 12, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-09-242-890-12

Query Match      17.4%; Score 39; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
Db 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQI 106
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RESULT 9
US-09-242-890-14
; Sequence 14, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Human
US-09-242-890-14

Query Match 16.5%; Score 37; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.6e-30; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0;
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVG 37
Db 1 MPCRPLRTVPGALGAWLLGGLWAWTLGGLCSLGAVG 37

RESULT 10
US-09-242-890-5
; Sequence 5, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse ependymin
US-09-242-890-5

Query Match 14.3%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.8e-25; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;
QY 105 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 136
Db 1 QIDQATKQCSKMTLTQPDPLDIPQNSTFEDQ 32

RESULT 11
US-09-242-890-3
; Sequence 3, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-3

Query Match 14.3%; Score 32; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.5e-24; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;
QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99
Db 31 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 62

RESULT 12
US-09-242-890-13
; Sequence 13, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 13
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mouse
US-09-242-890-13

Query Match 14.3%; Score 32; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.8e-24; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;
QY 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99
Db 68 SYDGLNQRVRLDERKALIPCKRLFEYILLYK 99

RESULT 13
US-09-242-890-9
; Sequence 9, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 9
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human and rat ependymin-like P

Query Match 11.6%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e-19; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0;

Qy 121 PWDPLDIPQNSTFEDQYSIGGPQEQI 146
Db 1 PWDPLDIPQNSTFEDQYSIGGPQEQI 26

RESULT 14
US-09-242-890-6
; Sequence 6, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; PRIOR FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 6
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Common amino acid sequence between human, rat and mouse
; OTHER INFORMATION: ependymin-like protein

Query Match 11.2%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 SYETWIGIYTVKDCYPVQETFTINY 183
Db 1 SYETWIGIYTVKDCYPVQETFTINY 25

RESULT 15
US-09-242-890-15
; Sequence 15, Application US/09242890
; Patent No. 6613887
; GENERAL INFORMATION:
; APPLICANT: Ogi, Kasuhiro
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human
; US-09-242-890-15

Query Match 10.7%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.2e-17; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

Qy 1 MPCRAPLRTVPGALGAWLLGGLWA 24
Db 1 MPCRAPLRTVPGALGAWLLGGLWA 24

Search completed: June 10, 2006, 03:25:51
Job time : 51 secs

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OM protein - protein search, using sw model

Run on: June 10, 2006, 03:26:06 ; Search time 16 Seconds
(without alignments)
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Title: US-10-733-646-2
Perfect score: 224
Sequence: 1 MFCRAFLRTVPGALWLLG.....TPPSTCQMAQLEKMSDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 64916 seqs, 12643201 residues

Word size : 1

Total number of hits satisfying chosen parameters: 64889

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	3.1	365	US-10-471-571A-558	Sequence 558, App
2	7	3.1	1866	US-10-511-937-2968	Sequence 2968, App
3	6	2.7	39	US-10-953-349-25806	Sequence 25806, A
4	6	2.7	118	US-10-370-959-111	Sequence 111, App
5	6	2.7	166	US-10-953-349-16478	Sequence 16478, A
6	6	2.7	166	US-10-953-349-19213	Sequence 19213, A
7	6	2.7	166	US-10-953-349-20109	Sequence 20109, A
8	6	2.7	166	US-10-953-349-23529	Sequence 23529, A
9	6	2.7	188	US-10-953-349-34495	Sequence 34495, A
10	6	2.7	201	US-10-953-349-31844	Sequence 31844, A
11	6	2.7	209	US-10-370-959-110	Sequence 110, App
12	6	2.7	231	US-10-471-571A-1786	Sequence 1786, App
13	6	2.7	238	US-10-953-349-31180	Sequence 31180, A
14	6	2.7	255	US-10-953-349-38691	Sequence 38691, A
15	6	2.7	256	US-10-953-349-1546	Sequence 1546, App
16	6	2.7	259	US-10-953-349-16938	Sequence 16938, A
17	6	2.7	262	US-11-293-697-4404	Sequence 4404, App
18	6	2.7	270	US-10-471-571A-2976	Sequence 2976, App
19	6	2.7	276	US-10-953-349-16477	Sequence 16477, A
20	6	2.7	276	US-10-953-349-19212	Sequence 19212, A
21	6	2.7	276	US-10-953-349-20108	Sequence 20108, A
22	6	2.7	276	US-10-953-349-23528	Sequence 23528, A
23	6	2.7	289	US-10-953-349-16937	Sequence 16937, A
24	6	2.7	300	US-11-264-737-101	Sequence 101, App
25	6	2.7	300	US-11-264-737-103	Sequence 103, App

26	6	2.7	303	6	US-10-953-349-18508	Sequence 18508, A
27	6	2.7	310	6	US-10-953-349-26321	Sequence 26321, A
28	6	2.7	310	6	US-10-953-349-38690	Sequence 38690, A
29	6	2.7	313	6	US-10-953-349-13557	Sequence 13557, A
30	6	2.7	314	6	US-10-538-066-365	Sequence 365, App
31	6	2.7	314	6	US-10-538-066-366	Sequence 366, App
32	6	2.7	320	6	US-10-953-349-18507	Sequence 18507, A
33	6	2.7	323	6	US-10-953-349-26320	Sequence 26320, A
34	6	2.7	325	6	US-10-953-349-38689	Sequence 38689, A
35	6	2.7	330	6	US-10-953-349-13556	Sequence 13556, A
36	6	2.7	332	6	US-10-953-349-28936	Sequence 28936, A
37	6	2.7	345	6	US-10-471-571A-1852	Sequence 1852, App
38	6	2.7	349	6	US-10-953-349-28935	Sequence 28935, A
39	6	2.7	358	6	US-10-953-349-30698	Sequence 30698, A
40	6	2.7	358	6	US-10-953-349-31887	Sequence 31887, A
41	6	2.7	359	6	US-10-953-349-26319	Sequence 26319, A
42	6	2.7	385	6	US-10-953-349-15764	Sequence 15764, A
43	6	2.7	385	6	US-10-953-349-16936	Sequence 16936, A
44	6	2.7	397	6	US-10-953-349-15763	Sequence 15763, A
45	6	2.7	430	6	US-10-953-349-21326	Sequence 21326, A

ALIGNMENTS

RESULT 1
US-10-471-571A-558
; Sequence 558, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 558
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(365)
; OTHER INFORMATION: Xaa-Pro dipeptidase
US-10-471-571A-558

Query Match 3.1%; Score 7; DB 6; Length 365;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 IDQATKQ 112
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Db 68 IDQATKQ 74

RESULT 2
US-10-511-937-2968
; Sequence 2968, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2968
; LENGTH: 1866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2968

Query Match          3.1%; Score 7; DB 6; Length 1866;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 ALGAWLL 19
Db      1810 ALGAWLL 1816

RESULT 3
US-10-953-349-25806
; Sequence 25806, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25806
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-25806

Query Match          2.7%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      206 PPSTCQ 211
Db      32 PPSTCQ 37

RESULT 4
US-10-370-959-111
; Sequence 111, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170NNIM
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; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-111

Query Match          2.7%; Score 6; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      82 RKALIP 87
Db      111 RKALIP 116

RESULT 5
US-10-953-349-16478
; Sequence 16478, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16478
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16478

Query Match          2.7%; Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7

RESULT 6
US-10-953-349-19213
; Sequence 19213, Application US/10953349
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19213
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19213

Query Match      2.7%  Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7
      |||||

RESULT 7
US-10-953-349-20109
; Sequence 20109, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20109
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-20109

Query Match      2.7%  Score 6; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7
      |||||

RESULT 8
US-10-953-349-23529
; Sequence 23529, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23529
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23529

Query Match      2.7%  Score 6; DB 6; Length 166;
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Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 LGAVGA 38
Db      2 LGAVGA 7
      |||||

RESULT 9
US-10-953-349-34495
; Sequence 34495, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34495
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34495

Query Match      2.7%  Score 6; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 LCGLCS 32
Db      36 LCGLCS 41
      |||||

RESULT 10
US-10-953-349-31844
; Sequence 31844, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31844
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31844

Query Match      2.7%  Score 6; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GRAPLR 8
Db      91 GRAPLR 96
      |||||

RESULT 11
US-10-370-959-110
; Sequence 110, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
```

```
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170NMIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-370-959-110
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Query Match 2.7%; Score 6; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 82 RKALIP 87
Db 201 RKALIP 206
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RESULT 12
US-10-471-571A-1786
; Sequence 1786, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1786
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(231)
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; OTHER INFORMATION: exotoxin 8 [Staphylococcus
US-10-471-571A-1786
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Query Match 2.7%; Score 6; DB 6; Length 231;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 136 QYSIGG 141
Db 114 QYSIGG 119
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RESULT 13
US-10-953-349-31180
; Sequence 31180, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31180
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31180
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Query Match 2.7%; Score 6; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 GRAPLR 8
Db 145 GRAPLR 150
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RESULT 14
US-10-953-349-38691
; Sequence 38691, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38691
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38691
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Query Match 2.7%; Score 6; DB 6; Length 255;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 65 ALLSYD 70
Db 95 ALLSYD 100
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RESULT 15
US-10-953-349-1546
; Sequence 1546, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1546
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1546

Query Match 2.7%; Score 6; DB 6; Length 256;
Best Local Similarity 100.0%; Pred.No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 LYKDG 102
Db 127 LYKDG 132

Search completed: June 10, 2006, 03:29:24
Job time : 17 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 03:25:10 ; Search time 184 Seconds
(without alignments)
563.914 Million cell updates/sec

Title: US-10-733-646-2

Perfect score: 224

Sequence: 1 MPCRPLRTVPGALGAWLLG.....TPPSTCQMAQLEKMSDCSW 224

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 3: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pcp.*
- 4: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	224	100.0	224	4	US-10-612-788-11
2	224	100.0	224	4	US-10-733-646-2
3	224	100.0	224	5	US-10-733-646-2
4	200	89.3	200	4	US-10-612-788-10
5	187	83.5	187	4	US-10-612-788-1
6	39	17.4	39	4	US-10-612-788-8
7	39	17.4	190	4	US-10-612-788-2
8	39	17.4	224	4	US-10-612-788-12
9	37	16.5	37	4	US-10-612-788-14
10	32	14.3	32	4	US-10-612-788-5
11	32	14.3	187	4	US-10-612-788-3
12	32	14.3	224	4	US-10-612-788-13
13	26	11.6	26	4	US-10-612-788-9
14	25	11.2	25	4	US-10-612-788-6
15	24	10.7	24	4	US-10-612-788-15
16	17	7.6	17	4	US-10-612-788-7
17	13	5.8	13	4	US-10-612-788-4
18	9	4.0	870	4	US-10-437-963-172504
19	9	4.0	1077	4	US-10-437-963-172507
20	9	4.0	1408	4	US-10-437-963-172498
21	8	3.6	8	5	US-10-997-519-12
22	8	3.6	8	5	US-10-997-519-14
23	8	3.6	598	4	US-10-195-144-29
24	8	3.6	598	4	US-10-345-072-29
25	7	3.1	34	4	US-10-612-788-16
26	7	3.1	67	4	US-10-424-599-143675
27	7	3.1	73	4	US-10-424-599-279297

28 7 3.1 79 4 US-10-424-599-235015 Sequence 235015,
29 7 3.1 117 4 US-10-437-963-117184 Sequence 117184,
30 7 3.1 120 4 US-10-425-115-289504 Sequence 289504,
31 7 3.1 142 5 US-10-617-320-5033 Sequence 5033, Ap
32 7 3.1 145 4 US-10-424-599-256370 Sequence 256370,
33 7 3.1 148 4 US-10-338-083-4 Sequence 4, Appli
34 7 3.1 148 4 US-10-611-399-4 Sequence 4, Appli
35 7 3.1 148 5 US-10-794-751-4 Sequence 9, Appli
36 7 3.1 158 4 US-10-170-812-9 Sequence 4400, A
37 7 3.1 191 4 US-10-282-122A-44400 Sequence 31, Appl
38 7 3.1 204 4 US-10-468-161-31 Sequence 31, Appl
39 7 3.1 204 5 US-10-982-442A-31 Sequence 31, Appl
40 7 3.1 204 6 US-11-136-341A-31 Sequence 39, Appl
41 7 3.1 208 3 US-09-027-287-39 Sequence 39, Appl
42 7 3.1 208 3 US-09-252-656B-39 Sequence 39, Appl
43 7 3.1 208 4 US-10-375-680-39 Sequence 39, Appl
44 7 3.1 208 5 US-10-943-197-4 Sequence 4, Appli
45 7 3.1 215 4 US-10-437-963-162234 Sequence 162234,

ALIGNMENTS

RESULT 1

US-10-612-788-11
; Sequence 11, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1 Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 224
; TYPE: PRT
; ORGANISM: human
US-10-612-788-11

Query Match 100.0%; Score 224; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSGAVCAPRCPQAPQOEGRWVYQSSG 60
DB 1 MPCRPLRTVPGALGAWLLGGLWAWTLGCLSGAVCAPRCPQAPQOEGRWVYQSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKELFYLLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKELFYLLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPQNSTFEDQYISGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180
DB 121 PWDPLDIPQNSTFEDQYISGGPQEQITVQWSDRKSARSYETWIGITVTKDCYPVQETFT 180
QY 181 INYSVILSTRFFDIQILGKIDPSVFTPTSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFFDIQILGKIDPSVFTPTSTCQMAQLEKMSDCSW 224

RESULT 2

US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20040122215A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.

```
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 224; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224

Query Match      100.0%; Score 224; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224

RESULT 3
US-10-733-646-2
; Sequence 2, Application US/10733646
; Publication No. US20050197491A9
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Human Ependymin
; FILE REFERENCE: PF403D2
; CURRENT APPLICATION NUMBER: US/10/733,646
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 10/187,904
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 09/229,583
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,330
; PRIOR FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: US 60/075,278
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-646-2

Query Match      100.0%; Score 224; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
DB 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
DB 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
DB 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
DB 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
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Db 1 MFCRAPLRTVPGALGAWLLGGLWAWTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSG 60
QY 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
Db 61 RNSRALLSYDGLNQRVRLDERKALIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQ 120
QY 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
Db 121 PWDPLDIPONSTFEDQYSIGGPQEQITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFT 180
QY 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224
Db 181 INYSVILSTRFRFDIQLGIKDPSPVFTPPSTCQMAQLEKMSDCSW 224

RESULT 4
US-10-612-788-10
; Sequence 10, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1e1 Human Ependymin-like Protein
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: human
US-10-612-788-10

Query Match      89.3%; Score 200; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.7e-189;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 WTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSGRNRRALLSYDGLNQRVRLDERKA 84
Db 1 WTLGCLSLGAVGAPRPPCOAPQOWEGROVMYQOSSGRNRRALLSYDGLNQRVRLDERKA 60
QY 85 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 144
Db 61 LIPCKRLFEYILLYKDGVMFQIDQATKQCSKMTLTQPDPLDIPQNSTFEDQYSIGGPQE 120
QY 145 QITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFRFDIQLGIKDPSPV 204
Db 121 QITVQEWSDRKSARSYETWIGIYTVKDCYPVQETFTINYSVILSTRFRFDIQLGIKDPSPV 180
QY 205 TTPSTCQMAQLEKMSDCSW 224
Db 181 TTPSTCQMAQLEKMSDCSW 200

RESULT 5
US-10-612-788-1
; Sequence 1, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1e1 Human Ependymin-like Protein
; FILE REFERENCE: 2417USIP
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
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; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-788-1

Query Match 83.5%; Score 187; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 5.6e-176; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 APRPCAPQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYILL 97
Db 1 APRPCAPQWEGRQVMYQSSGRNSRALLSYDGLNQRVRLDERKALIPCKRLFYILL 60
QY 98 YKGVNFQIDQATKQCSKMTLTQWDFDLIPQNSTFEDQYSIGPQEQITVQWSDRKS 157
Db 61 YKGVNFQIDQATKQCSKMTLTQWDFDLIPQNSTFEDQYSIGPQEQITVQWSDRKS 120
QY 158 RSVETWIGIVTVKDCVPQVQETFTINYSVILSTRFFDIQLGKDPVSFTPBSTCOMAQLEK 217
Db 121 RSVETWIGIVTVKDCVPQVQETFTINYSVILSTRFFDIQLGKDPVSFTPBSTCOMAQLEK 180
QY 218 MSDEDCSW 224
Db 181 MSDEDCSW 187

RESULT 6
US-10-612-788-8
; Sequence 8, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 39
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-8

Query Match 17.4%; Score 39; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e-30; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106
Db 1 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 39

RESULT 7
US-10-612-788-2
; Sequence 2, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02

; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-2

Query Match 17.4%; Score 39; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 6.6e-30; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106
Db 34 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 72

RESULT 8
US-10-612-788-12
; Sequence 12, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rat
US-10-612-788-12

Query Match 17.4%; Score 39; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.6e-30; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106
Db 68 SYDGLNQRVRLDERKALIPCKRLFYILLYKGVNMFQI 106

RESULT 9
US-10-612-788-14
; Sequence 14, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
US-10-612-788-14


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; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 25
; TYPE: PRT
; ORGANISM: mammalian
US-10-612-788-6
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Query Match 11.2%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 159 SYETWIGIYTKDCYPVQETFTNY 183
Db 1 SYETWIGIYTKDCYPVQETFTNY 25
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RESULT 15
US-10-612-788-15
; Sequence 15, Application US/10612788
; Publication No. US20040014947A1
; GENERAL INFORMATION:
; APPLICANT: OGI, Kazuhiro
; APPLICANT: ONDA, Haruo
; TITLE OF INVENTION: No. US20040014947A1el Human Ependymin-like Protein
; FILE REFERENCE: 2417US1P
; CURRENT APPLICATION NUMBER: US/10/612,788
; CURRENT FILING DATE: 2003-07-02
; PRIOR APPLICATION NUMBER: 09/242,890
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human
US-10-612-788-15
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Query Match 10.7%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPGRAPLRTVPGALGAWLLGGLWA 24
Db 1 MPGRAPLRTVPGALGAWLLGGLWA 24
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Search completed: June 10, 2006, 03:29:01
Job time : 185 secs
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